

QY 1 MAAPVEDNCINFVAMKFIDNTLYFIABDDENLESD 36
DB 1 MAAPVEDNCINFVAMKFIDNTLYFIABDDENLESD 36

RESULT 2

US-08-896-501A-1
Sequence 1, Application US/08896501A
Patent No. 5891663
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,501A
FILING DATE: 18-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 31,474/1997
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO=3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal fragment
US-08-896-501A-1

Query Match 100.0%; Score 188; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 3.4e-21;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIDNTLYFIABDDENLESD 36
DB 1 MAAPVEDNCINFVAMKFIDNTLYFIABDDENLESD 36

RESULT 3
US-08-896-605A-2
Sequence 2, Application US/08896605A
Patent No. 5879942
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,605A
FILING DATE: 18 JULY 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207,691/1996
FILING DATE: 19-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 156,062/1997
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-896-605A-2

Query Match 100.0%; Score 188; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIDNTLYFIABDDENLESD 36
DB 1 MAAPVEDNCINFVAMKFIDNTLYFIABDDENLESD 36

RESULT 4
US-08-896-501A-2
Sequence 2, Application US/08896501A
Patent No. 5891663
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,501A
FILING DATE: 18-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 213,267/1996
FILING DATE: 25-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 31,474/1997

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OM protein - protein search, using SW model

Run on: May 13, 2005, 12:17:10 / Search time 42 Seconds
(without alignments)
63.985 Million cell updates/sec

Title: US-09-711-896A-1

Perfect score: 188

Sequence: 1 MAAPEDNCFVAMKPIDNTLYIAEDDENLSD 36

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents AA:
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2: /cgn2_6/prodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep.*
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5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/1aa/Backfillseq1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	188	100.0	41 2 US-08-896-501A-1	Sequence 1, Appl
3	188	100.0	193 2 US-08-896-605A-2	Sequence 2, Appl
4	188	100.0	193 3 US-08-896-501A-2	Sequence 2, Appl
5	188	100.0	193 3 US-08-832-180-9	Sequence 4, Appl
6	188	100.0	193 4 US-10-105-080-4	Sequence 9, Appl
7	188	100.0	193 4 US-09-949-016-6095	Sequence 6095, Ap
8	179	95.2	193 4 US-09-597-576-2	Sequence 2, Appl
9	139.5	74.2	133 4 US-09-817-265A-2	Sequence 2, Appl
10	139.5	74.2	192 4 US-09-917-265A-8	Sequence 8, Appl
11	132	70.2	193 4 US-09-445-724B-2	Sequence 2, Appl
12	132	70.2	193 4 US-09-445-724B-6	Sequence 6, Appl
13	110	58.5	192 4 US-10-105-080-5	Sequence 5, Appl
14	50	26.6	78 4 US-09-749-637A-318	Sequence 318, App
15	50	26.6	536 4 US-08-653-648A-13	Sequence 13, Appl
16	50	26.6	536 4 US-09-564-418-9	Sequence 13, Appl
17	49.5	26.3	569 4 US-09-107-532A-6689	Sequence 6689, Ap
18	49	26.1	78 4 US-09-248-796A-27329	Sequence 27329, A
19	49	26.1	367 4 US-09-134-000C-6071	Sequence 6071, Ap
20	49	26.1	747 3 US-08-089-397A-15	Sequence 15, Appl
21	49	26.1	776 1 US-07-603-133B-17	Sequence 17, Appl
22	49	26.1	776 1 US-07-603-133B-20	Sequence 20, Appl
23	49	26.1	776 1 US-08-089-397A-15	Sequence 15, Appl
24	48.5	25.8	464 1 US-07-991-867B-2	Sequence 2, Appl
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27	48.5	25.8	464 4 US-09-370-861A-2	Sequence 2, Appl

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30	48	25.5	688 3 US-09-113-750A-3	Sequence 3, Appl
31	47.5	25.3	1039 4 US-09-328-352-5474	Sequence 5474, Ap
32	47.5	25.3	1806 4 US-09-919-497-56	Sequence 56, Appl
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35	47	25.0	546 4 US-09-746-359A-37	Sequence 37, Appl
36	47	25.0	694 2 US-08-895-522-4	Sequence 4, Appl
37	47	25.0	694 3 US-09-195-391-4	Sequence 15, Appl
38	47	25.0	775 1 US-07-603-133B-15	Sequence 15, Appl
39	47	25.0	775 1 US-07-603-133B-16	Sequence 16, Appl
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45	46	24.5	266 3 US-09-414-276-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-896-605A-1
Sequence 1, Application US/08896605A
Patent No. 5879942
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INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal fragment
US-08-896-605A-1
Query Match 100.0%; Score 188; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 3.4e-21;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RT "African swine fever virus encodes a CP2 homolog responsible for the
 RT adhesion of erythrocytes to infected cells.";
 RL J. Virol. 67:5312-5320(1993).
 RN [18]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93277388; PubMed=8503790;
 RA Munoz M., Freije J.M., Salas M.L., Vinuela E., Lopez-Otin C.;
 RT "Structure and expression in E. coli of the gene coding for protein
 RT p10 of African swine fever virus.";
 RL Arch. Virol. 130:93-107(1993).
 RN [19]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=94065656; PubMed=8245848;
 RA Alcantar A., Angulo A., Vinuela E.;
 RT "Mapping and sequence of the gene encoding the African swine fever
 RT virion protein of M(r) 11500.";
 RL J. Gen. Virol. 74:2317-2324(1993).
 RN [20]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=9413396; PubMed=8293992; DOI=10.1016/0378-1119(93)90453-A;
 RA Rodriguez J.M., Yanez R.J., Rodriguez J.F., Vinuela E., Salas M.L.;
 RT "The DNA polymerase-encoding gene of African swine fever virus:
 RT sequence and transcriptional mapping.";
 RL Gene 136:103-110(1993).
 RN [21]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=94187118; PubMed=8139051;
 RA Rodriguez J.M., Yanez R.J., Pan R., Rodriguez J.F., Salas M.L.,
 RL Vinuela E.;
 RT "Multigene families in African swine fever virus: family 505.";
 RL J. Virol. 68:2746-2751(1994).
 RN [22]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=94233765; PubMed=8178480;
 RA De la Vega I., Gonzalez A., Blasco R., Calvo V., Vinuela E.;
 RT "Nucleotide sequence and variability of the inverted terminal
 RT repetitions of African swine fever virus DNA.";
 RL Virology 201:152-156(1994).
 RN [23]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=91820291; PubMed=11831707;
 RA Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C.,
 RT Rodriguez J.F., Vinuela E.;
 RT "Analysis of the complete nucleotide sequence of African swine fever
 RT virus.";
 RL Virology 208:249-278(1995).
 RN [24]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
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 DB Best Local Similarity 27.3%; Pred. No. 1.5e+02;
 Matches 12; Conservative 8; Mismatches 15; Indels 9; Gaps 1;

GN Name=dapE;
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteriaceae; Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P37;
 RX MEDLINE=95331541; PubMed=7607469; DOI=10.1016/0378-1119(94)00668-I;
 RA Vitor J.M., Morgan R.D.;
 RT "Two novel restriction endonucleases from Campylobacter jejuni.";
 RL Gene 157:109-110(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P37;
 RA Vitor J.M.B.;
 RT "Restriction and modification systems in Campylobacter jejuni and C.
 RT coli.";
 RL Thesis (1999), University of Lisbon, Lisbon, Portugal.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P37;
 RA Vitor J.M.B.;
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF264911; AAF77191.1; -;
 DR InterPro: IPR001261; ARGB dapE.
 DR PROSITE: PS00758; ARGB_DAPF_CPG2_1; UNKNOWN_1.
 FT NON TER 70 70
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 DB 17 PNDGALNFIAMELSDFEAFPIEKE 41
 QY Query Match 28.2%; Score 53; DB 2; Length 99;
 DB Best Local Similarity 27.3%; Pred. No. 1.1;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 DB 79 ETLRDNAIFVARKOLENKY 99
 QY Query Match 28.2%; Score 53; DB 2; Length 99;
 DB Best Local Similarity 27.3%; Pred. No. 1.1;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 DB 79 ETLRDNAIFVARKOLENKY 99
 Search completed: May 13, 2005, 12:25:11
 Job time : 177 sec

065146 ID 065146 PRELIMINARY; PRT; 1055 AA.
 AC 065146;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
 DE Helicase.
 GN Name=PI055L;
 OS African swine fever virus (ASFV).
 OC Viruses; dsDNA viruses, no RNA stage; Asfarviridae; Asfivirus.
 OX NCBI_TaxId=10497;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=90223993; PubMed=2327074;
 RA Lopez-Otin C., Freije J.M.P., Parra F., Mendez E., Vinnela E.;
 RT "Mapping and sequence of the gene coding for protein p72, the major
 RL capsid protein of African swine fever virus."; Virol. 175:477-484(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=90357780; PubMed=2389555;
 RA Blasco R., Lopez-Otin C., Munoz M., Bockamp E.-O., Simon-Mateo C.,
 RA Vinnela E.;
 RT "Sequence and evolutionary relationships of African swine fever virus
 RL thymidine kinase."; Virol. 178:301-304(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=90219204; PubMed=2325202;
 RA Alendral J.M., Almazan F., Blasco R., Vinnela E.;
 RT "Multigene families in African swine fever virus: family 110."; Virol. 64:2064-2072(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=90219205; PubMed=2325203;
 RA Gonzalez A., Calvo V., Almazan F., Alendral J.M., Ramirez J.C.,
 RA De La Vega I., Blasco R., Vinnela E.;
 RT "Multigene families in African swine fever virus: family 360."; Virol. 64:2073-2081(1990).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=91134988; PubMed=1994575;
 RA Camacho A., Vinnela E.;
 RT "Protein p22 of African swine fever virus: an early structural protein
 RL that is incorporated into the membrane of infected cells."; Virol. 181:251-257(1991).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=92087485; PubMed=1309282;
 RA Rodriguez J.M., Salas M.L., Vinnela E.;
 RT "Genes homologous to ubiquitin-conjugating proteins and eukaryotic
 RL transcription factor SII in African swine fever virus."; Virol. 186:40-52(1992).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93174976; PubMed=8438592;
 RA Yanez R.J., Vinnela E.;
 RT "African swine fever virus encodes a DNA ligase."; Virol. 193:531-536(1993).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=92263807; PubMed=1316688;
 RA Garcia-Beato R., Freije J.M.P., Lopez-Otin C., Blasco R., Vinnela E.,
 RA Salas M.L.;
 RT "A gene homologous to topoisomerase II in African swine fever virus.";

RL Virol. 188:938-947(1992).
 RN [9]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=92260660; PubMed=1583732;
 RA Alcant A., Angulo A., Lopez-Otin C., Munoz M., Freije J.M.P.,
 RA Carrascosa A.L., Vinnela E.;
 RT "Amino acid sequence and structural properties of protein p12, an
 RL African swine fever virus attachment protein."; Virol. 66:3860-3868(1992).
 RN [10]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=94091056; PubMed=8266720; DOI=10.1016/0168-1702(93)90016-G;
 RA Freije J.M., Iain S., Vinnela E., Lopez-Otin C.;
 RT "Nucleotide sequence of a nucleoside triphosphate phosphohydrolase
 RL gene from African swine fever virus."; Virus Res. 30:63-72(1993).
 RN [11]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93346971; PubMed=8393914;
 RA Yanez R.J., Rodriguez J.M., Rodriguez J.F., Salas M.L., Vinnela E.;
 RT "African swine fever virus thymidylate kinase gene: sequence and
 RL transcriptional mapping."; J. Gen. Virol. 74:1633-1638(1993).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93281390; PubMed=8506138;
 RA Yanez R.J., Boursnell M., Nogal M.L., Yuste L., Vinnela E.;
 RT "African swine fever virus encodes two genes which share significant
 RL homology with the two largest subunits of DNA-dependent RNA
 RN polymerases."; Nucleic Acids Res. 21:2423-2427(1993).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93174941; PubMed=8382399;
 RA Pena L., Yanez R.J., Revilla Y., Vinnela E., Salas M.L.;
 RT "African swine fever virus guanylyltransferase."; Virol. 193:319-328(1993).
 RN [14]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93327788; PubMed=8335009;
 RA Simon-Mateo C., Andres G., Vinnela E.;
 RT "Polyprotein processing in African swine fever virus: a novel gene
 RL expression strategy for a DNA virus."; EMBO J. 12:2977-2987(1993).
 RN [15]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93233210; PubMed=8474154;
 RA Prados F.J., Vinnela E., Alcant A.;
 RT "Sequence and characterization of the major early phosphoprotein p32
 RL of African swine fever virus."; J. Virol. 67:2475-2485(1993).
 RN [16]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=94085774; PubMed=8262374; DOI=10.1016/0378-1119(93)90090-P;
 RA Yanez R.J., Rodriguez J.M., Boursnell M.E.G., Rodriguez J.F.,
 RA Vinnela E.;
 RT "Two putative African swine fever virus helicases similar to yeast
 RL 'DBP' pre-mRNA processing proteins and vaccinia virus ATPases D1L
 and D6R."; Gene 134:161-174(1993).
 RN [17]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE=93353606; PubMed=8102411;
 RA Yanez R.J., Almazan F., Vinnela E., Rodriguez J.F.;

QY 5 PVED-----NCINPAMKPIDNTLYPIAEDDENTLE 34
 DB 161 PVEDVNCIFQGCRCPRFISCEPAHNNNSWYTFESDEDAQ 199

RESULT 35

Q96410 PRELIMINARY; PRT; 417 AA.
 AC 096410, 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Serum response factor.
 GN Name=SRF;
 OS Hydra attenuata (Hydra) (Hydra vulgaris).
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroids; Anthomedusae;
 CC Hydridae; Hydra.
 CX NCBI_TaxId=6087;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21369530; PubMed=11476573; DOI=10.1006/dbio.2001.0335;
 RA Hoffmann U., Krolner M.;
 RT "A possible role for the chidarian homologue of serum response factor
 in decision making by undifferentiated cells."
 RL Dev. Biol. 236:304-315 (2001).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL: AF306544; AAK81817.1; -.
 DR HSP; P11831; IHEX.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; P:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
 DR InterPro: IPR002100; TF_MADSbox.
 DR Pfam: PF00319; SRF-TF; 1
 DR PRINTS: PR00404; MADSBOXMIN.
 DR SMART: SM00432; MADS_1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS0066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 KW SEQUENCE 417 AA; 47097 MW; 4E916EB15605515 CRC64;

Query Match 28.7%; Score 54; DB 2; Length 417;
 Best Local Similarity 35.5%; Pred. No. 43;
 Matches 11; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 6 VEDNCINPAMKPIDNTLYPIAEDDENTLESD 36
 DB 42 VEDTHLSFVQPLIVBETKHYOSLDEDLTD 72

RESULT 36

Q7Y256 PRELIMINARY; PRT; 921 AA.
 AC 07Y256, 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Ubiquitin-specific protease, probable.
 GN ORFNames=IMB.672;
 OS Cryptosporidium parvum.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 CC Cryptosporidiidae; Cryptosporidium.
 CX NCBI_TaxId=5807;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Bankler A.T., Spirigs H.F., Partmann B., Konfortov B.A., Madera M.,
 Vogel C., Teichmann S.A., Ivens A., Dear P.H.;
 RT "Integrated mapping, chromosomal sequencing and sequence analysis of
 Cryptosporidium parvum."
 RL Genome Res. 0:0-0(2003).
 DR EMBL: BX53853; CAD98271.1; -.
 DR GO: GO:0004197; P:cysteine-type endopeptidase activity; IEA.

DR GO: GO:0008233; F:peptidase activity; IEA.
 DR GO: GO:0004221; F:ubiquitin thiolesterase activity; IEA.
 DR GO: GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
 DR InterPro: IPR001394; Peptidase_C19.
 DR InterPro: IPR00449; UBA.
 DR InterPro: IPR01607; ZnF_UBP.
 DR Pfam: PF00443; UCH_1.
 DR Pfam: PF02148; ZF_UBP_1.
 DR SMART: SM0165; UBA_1.
 DR PROSITE: PS0030; UBA_1.
 DR PROSITE: PS00972; UCH_2_1; 1.
 DR PROSITE: PS00973; UCH_2_2; 1.
 DR PROSITE: PS0235; UCH_2_3; 1.
 DR Protease.
 KW SEQUENCE 921 AA; 104507 MW; 9447C853FF572F67 CRC64;

Query Match 28.7%; Score 54; DB 2; Length 921;
 Best Local Similarity 33.3%; Pred. No. 1.1e+02;
 Matches 9; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 4 BEVEDNCINPAMKPIDNTLYPIAEDD 30
 DB 879 QPTSSCSSIWRNDIKYLSKEDD 905

RESULT 37

Q86A22 PRELIMINARY; PRT; 494 AA.
 AC 086A22, 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Similar to Gallus gallus (Chicken). Cytochrome P-450.
 CC Dictyostelium discoideum (slime mold).
 OS Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 CX NCBI_TaxId=44689;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RX MEDLINE=22092822; PubMed=12097910; DOI=10.1038/nature00847;
 RA Glockner G., Richinger L., Szefranek K., Pachter J., Dear P.,
 Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
 Tunggal B., Cox B., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."
 RL Nature 418:79-85(2002).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Baumgart C.;
 RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 DR EMBL: AC117175; AA052115.1; -.
 DR GO: GO:0004497; F:monooxygenase activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR01128; Cytochrome_P450.
 DR InterPro: IPR02401; EP450I.
 DR Pfam: PF00067; P450_1.
 DR PRINTS: PR00463; EP450I.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
 DR Heme; Monooxygenase; Oxidoreductase.
 KW SEQUENCE 494 AA; 57571 MW; 26BCA28F2ED2486E CRC64;

Query Match 28.5%; Score 53.5; DB 2; Length 494;
 Best Local Similarity 44.0%; Pred. No. 62;
 Matches 11; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 8 DNCINPAMKPIDNTLYPIAEDD 32
 DB 248 NNCINP-QPLIDNLIKNSIDDDDD 271

RESULT 38

RC STRAIN-S288C / AB972;
 RX MEDLINE-95249563; PubMed-7731988;
 RA Bussey H., Kadack D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
 RA Hall J., Ouellette B.F.P., Keng T., Barton A.B., Su Y., Davies C.K.,
 RA Storms R.K.;
 RT "The nucleotide sequence of chromosome I from *Saccharomyces*
 RT *cerevisiae*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
 CC -1- FUNCTION: Involved in the transfer of acetyl-CoA into
 CC mitochondria. May also be involved in the metabolism of acetate
 CC and of ethanol.
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + carnitine = CoA + O-
 CC acetylcarbitine.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane; outer side.
 CC -1- INDUCTION: By ethanol and by acetate. Repressed by glucose, and to
 CC a lesser extent, by galactose. Derepressed by glycerol.
 CC -1- SIMILARITY: Belongs to the carnitine/choline acetyltransferase
 CC family.

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 CC or send an email to license@isb-sib.ch).

 CC
 DR EMBL: X74553; CAA52647.1; -;
 DR EMBL: L28920; AAC09495.1; -;
 DR PIR: S53485; S53485.
 DR HSSP: P47934; INDF.
 DR Germonline: J38421; -;
 DR SGD: S000000080; YAT1.
 DR GO: GO:0005739; C:mitochondrion; IDA.
 DR GO: GO:0006066; P:alcohol metabolism; IGI.
 DR GO: GO:0009437; P:carnitine metabolism; IMP.
 DR InterPro: IPR000542; Carn_acyl_trans.
 DR Pfam: PF00735; Carn_acyltransferase; 1.
 DR PROSITE: PS00439; ACYLTRANSF_C_1; FALSE_NEG.
 DR PROSITE: PS00440; ACYLTRANSF_C_2; 1.
 DR Kegg: K00000; Fatty acid metabolism; Mitochondrion; Transferase;
 KM Acyltransferase; Fatty acid metabolism; Mitochondrion; Transferase;
 KM Transport.
 FT ACT SITE 346 346 Potential.
 FT CONFLICT 25 25 T -> P (in Ref. 2).
 FT CONFLICT 393 393 Missing (in Ref. 2).
 FT CONFLICT 596 597 AS -> SF (in Ref. 2).
 FT CONFLICT 654 654 T -> A (in Ref. 2).
 FT CONFLICT 661 661 A -> T (in Ref. 2).
 SO SEQUENCE 688 AA; 77780 MW; 6445A08B59A5F64B CRC64;

 Qy Query Match 29.3%; Score 55; DB 1; Length 688;
 Best Local Similarity 34.5%; Pred. No. 55;
 Matches 10; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

 Db 8 DNCINPAMKFDINTLYFIADNLESD 36
 260 DDCTNWRNLKIDALFVCLDVAFAD 288

 RESULT 33
 ID 06CUT7 PRELIMINARY; PRT; 862 AA.
 AC 06CUT7;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Similar to *ca* |CA1657|IPF16022 *Candida albicans* unknown function.
 GN ORName=TLN0F160389;
 OS *Kluyveromyces fragilis* NRRL Y-1140.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; *Kluyveromyces*.
 OX NCBI_TaxID=284590;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG Genolevers;
 RA Dutton B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Nevegilis C., Talla E.,
 RA Gottard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barany S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Bolerame A., Boyer J., Catterico L., Confiantieri P., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hartrey F., Hennegou C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Kozul R., Lemaitre M., Lesur I., Ma L., Muller H.,
 RA Nicoud J.M., Nikolaki M., Oztas S., Ozler-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=NRRL Y-1140;
 RC Genoscope;
 RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 4 WD repeats.
 CC EMBL: CR382126; CAG98510.1; -;
 DR InterPro: IPR001680; WD40.
 DR InterPro: IPR011046; WD40_like.
 DR Pfam: PF04400; WD40; 4.
 DR SMART: SM00320; WD40; 7.
 DR Repeat; WD repeat.
 KM SEQUENCE 862 AA; 96845 MW; BF90B87AA74E1909 CRC64;

 Qy Query Match 29.3%; Score 55; DB 2; Length 862;
 Best Local Similarity 42.3%; Pred. No. 71;
 Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

 Db 4 EPVEDNCINPAMKFDINTLYFIAD 29
 552 ETVADNKNIGNIQLEMCKNLYTSSD 577

 RESULT 34
 ID 070SF7 PRELIMINARY; PRT; 439 AA.
 AC 070SF7;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE AGCP5851 (Fragment).
 GN Name=agc51593; ORName=ENSGANG00000011002;
 OS *Anopheles gambiae* str. F85T.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.
 OX NCBI_TaxID=180454;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL: AAB0100860; EA11778.1; -;
 DR InterPro: IPR006630; Lupus_La_dom.
 DR Pfam: PF05383; Ia; 1.
 FT NON_TER 1 1
 FT NON_TER 439 439
 SO SEQUENCE 439 AA; 45810 MW; 242AB05879D7B7ED CRC64;

 Qy Query Match 29.0%; Score 54.5; DB 2; Length 439;
 Best Local Similarity 33.3%; Pred. No. 39;
 Matches 13; Conservative 7; Mismatches 10; Indels 9; Gaps 2;

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=158679;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani-U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
 RA Kankiwa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus".
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AF003135; BAB42852.1; -
 DR GO; GO:0016787; P:hydrolyase activity; IEA.
 DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
 DR InterPro; IPR003089; AB_hydrolase.
 DR InterPro; IPR000379; Ser_estr.
 DR PRINTS; PRO011; ABHYDROLASE.
 DR Complete proteome.
 SK SEQUENCE 275 AA; 31865 MW; 22E950A39C18ABE1 CRC64;
 QY
 Db 4 EPEVNCINFMVKFID---NTLYFIAEDDENLE 34
 242 EPERDEVMRYI-LTFIANSVNTMGFIVEDEIVE 274
 RESULT 30
 ID 06G8G4 PRELIMINARY; PRT; 275 AA.
 AC 06G8G4
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=SA31689;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=282459;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsle K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 DR EMBL; BX571857; CA64392.1; -
 DR GO; GO:0016787; P:hydrolyase activity; IEA.
 DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
 DR InterPro; IPR003089; AB_hydrolase.
 DR InterPro; IPR000379; Ser_estr.
 DR PRINTS; PRO011; ABHYDROLASE.
 DR Complete proteome; Hypothetical protein.
 SK SEQUENCE 275 AA; 31865 MW; 22E950A39C18ABE1 CRC64;
 QY
 Db 4 EPEVNCINFMVKFID---NTLYFIAEDDENLE 34
 242 EPERDEVMRYI-LTFIANSVNTMGFIVEDEIVE 274
 Query Match 29.3%; Score 55; DB 2; Length 275;
 Best Local Similarity 38.2%; Pred. No. 19;
 Matches 13; Conservative 8; Mismatches 9; Indels 4; Gaps 2;

QY
 Db 4 EPEVNCINFMVKFID---NTLYFIAEDDENLE 34
 242 EPERDEVMRYI-LTFIANSVNTMGFIVEDEIVE 274
 RESULT 31
 ID 06GFT8 PRELIMINARY; PRT; 275 AA.
 AC 06GFT8
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=SA31689;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=282458;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsle K.,
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 DR EMBL; BX571856; CA640839.1; -
 DR GO; GO:0016787; P:hydrolyase activity; IEA.
 DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
 DR InterPro; IPR003089; AB_hydrolase.
 DR InterPro; IPR000379; Ser_estr.
 DR PRINTS; PRO011; ABHYDROLASE.
 DR Complete proteome; Hypothetical protein.
 SK SEQUENCE 275 AA; 31880 MW; 2358E0A22DA8ABE1 CRC64;
 QY
 Db 4 EPEVNCINFMVKFID---NTLYFIAEDDENLE 34
 242 EPERDEVMRYI-LTFIANSVNTMGFIVEDEIVE 274
 Query Match 29.3%; Score 55; DB 2; Length 275;
 Best Local Similarity 38.2%; Pred. No. 19;
 Matches 13; Conservative 8; Mismatches 9; Indels 4; Gaps 2;
 QY
 Db 4 EPEVNCINFMVKFID---NTLYFIAEDDENLE 34
 242 EPERDEVMRYI-LTFIANSVNTMGFIVEDEIVE 274
 RESULT 32
 ID CACM YEAST STANDARD; PRT; 688 AA.
 AC P80235;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Putative mitochondrial carnitine O-acetyltransferase (EC 2.3.1.7).
 GN Name=YAT1; OrderedLocustNames=VAR035W;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxId=4932;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX STRAIN=DL-1;
 RX MEDLINE=94086564; PubMed=8262985;
 RA Schmalix W., Bandlow W.,
 RT "The ethanol-inducible YAT1 gene from yeast encodes a presumptive
 RT mitochondrial outer carnitine acetyltransferase.";
 RL J. Biol. Chem. 268:27428-27439(1993).
 RN (2)
 SK SEQUENCE FROM N.A.

QY 7 EDNCINPFAVAKFIDNTLYFIA--EDDNLAS 35
 DB 303 EDNCYDIYERKKNNGNINIFCSFDYEDDNLTS 333

RESULT 26

ID 0873J5 PRELIMINARY; PRT; 1106 AA.
 AC 0873J5;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Probable ATP dependent RNA helicase.
 GN Name=89B11.040;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
 NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Altm V., Hehseisel J., Brandt P., Partmann B., Holland R.,
 RA Nykatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL/ BX284747; CAD70310.1; -
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO: GO:0016787; F:hydrolyase activity; IEA.
 DR GO: GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR01545; DEAD/DEAH N.
 DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; Helicase_C; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC_C; 1.
 KM ATP-binding; Helicase; Hydrolyase.
 SQ SEQUENCE 1106 AA; 124482 MW; B82262FFB78D22A2 CRC64;

QY Query Match 29.8%; Score 56; DB 2; Length 1106;
 Best Local Similarity 41.4%; Pred. No. 68;
 Matches 12; Conservative 6; Mismatches 7; Indels 4; Gaps 1;
 DB 5 PVEDNCINPFAVAKFIDNTLYFIADDENL 33
 468 PDEBNMWN---KVFENALASISDDKTL 492

RESULT 27

ID 0997A3 PRELIMINARY; PRT; 275 AA.
 AC 0997A3;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Lysophospholipase homolog.
 GN OrderedLocusNames=SAV1765;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunari H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus";

RL Lancet 357:1225-1240(2001).
 DR EMBL/ AP003363; BAB57927.1; -
 DR PIR/ G89961; G89961.
 DR GO: GO:0016787; F:hydrolyase activity; IEA.
 DR GO: GO:0006725; F:aromatic compound metabolism; IEA.
 DR InterPro: IPR003089; AB hydrolyase.
 DR InterPro: IPR000378; Ser_estrs.
 DR PRINTS: PRO0111; ABHYDROLASE.
 KM Complete proteome.
 SQ SEQUENCE 275 AA; 31865 MW; 22E950A39C18ABE1 CRC64;

QY Query Match 29.3%; Score 55; DB 2; Length 275;
 Best Local Similarity 38.2%; Pred. No. 19;
 Matches 13; Conservative 8; Mismatches 9; Indels 4; Gaps 2;

QY 4 EPEVDNCINPFAVAKFID--NTLYFIADDENL 34
 DB 242 EPERDEVMYRI-LTFINNSVNTGFIYEDDEIVE 274

RESULT 28

ID 07A0L7 PRELIMINARY; PRT; 275 AA.
 AC 07A0L7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE MM1706 protein.
 GN OrderedLocusNames=MM1706;
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Amano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA";
 RL Lancet 359:1819-1827(2002).
 DR EMBL/ AP004828; BAB5571.1; -
 DR GO: GO:0016787; F:hydrolyase activity; IEA.
 DR GO: GO:0006725; F:aromatic compound metabolism; IEA.
 DR InterPro: IPR003089; AB hydrolyase.
 DR InterPro: IPR000379; Ser_estrs.
 DR PRINTS: PRO0111; ABHYDROLASE.
 KM Complete proteome.
 SQ SEQUENCE 275 AA; 31865 MW; 22E950A39C18ABE1 CRC64;

QY Query Match 29.3%; Score 55; DB 2; Length 275;
 Best Local Similarity 38.2%; Pred. No. 19;
 Matches 13; Conservative 8; Mismatches 9; Indels 4; Gaps 2;

QY 4 EPEVDNCINPFAVAKFID--NTLYFIADDENL 34
 DB 242 EPERDEVMYRI-LTFINNSVNTGFIYEDDEIVE 274

RESULT 29

ID 07A5I3 PRELIMINARY; PRT; 275 AA.
 AC 07A5I3;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE SA1584 protein.
 GN OrderedLocusNames=SA1584;
 OS Staphylococcus aureus (strain N315).

FT NON_TER 1 1
 FT NON_TER 178 178
 SQ SEQUENCE 178 AA; 20631 MW; 816D6B2B88ACB497 CRC64;

Query Match
 Best Local Similarity 49.5%; Score 93; DB 2; Length 178;
 Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 16 MKPNDTLYPIADDDNTLESD 36
 DB 1 MKPNDTLYPIADDDNTLESD 21

RESULT 23
 ID 096244 PRELIMINARY; PRT; 1643 AA.

AC 096244; 01-MAY-1999 (TRENBLrel. 10, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein PF80755W.

OS Plasmodium falciparum (Isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=36329;

RP SEQUENCE FROM N.A.
 RX MEDLINE=99021743; PubMed=9804551; DOI=10.1126/science.282.5391.1126;

RA Gardner M.J., Tetteh H., Carucci D.J., Cummings L.M., Aravind L.,
 RA Koonin E.V., Shallow S., Mason T., Yu K., Fujii C., Peterson J.,
 RA Shen K., Jing J., Ascon C., Lai Z., Schwartz D.C., Perera M.,
 RA Salberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
 RA Frazer C.M., Adams M.D., Venter J.C., Hoffman S.L.,
 RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
 falciparum."
 RT Science 282:1126-1132(1998).

RL [2]
 RN SEQUENCE FROM N.A.

RA MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
 RA Gardner M.J., Hall N., Fung B., White O., Bertin M., Hyman R.W.,
 RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
 RA Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Angioli S.,
 RA Perera M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,
 RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Frazer C.M., Bartell B.,
 RT "Genome sequence of the human malaria parasite Plasmodium
 falciparum."
 RT Nature 419:498-511(2002).

DR EMBL; AE001416; AAC71940.2; --
 DR PIR; H71606; H71606.
 KM Hypothetical protein.
 SQ SEQUENCE 1643 AA; 19775 MW; DDD2A3B3746B419 CRC64;

Qy Query Match
 Best Local Similarity 33.2%; Score 62.5; DB 2; Length 1643;
 Matches 13; Conservative 8; Mismatches 11; Indels 9; Gaps 1;

Qy 4 EPVEDNCINFVAMKFI-----DNTLYPIADDDNTLESD 35
 DB 1045 EKDLACISYLSIKNIHIVIKMNDLFIITRDENIS 1085

RESULT 24
 ID 07R3W4 PRELIMINARY; PRT; 1153 AA.

AC 07R3W4; 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Dentin staphosphoprotein precursor.

GN Name=PY03111;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=73239;

RP SEQUENCE FROM N.A.
 RX STRAIN=17XNL;
 RX PubMed=12368865; DOI=10.1038/nature01099;

RA Carlton J.M., Angioli S.V., Suh B.B., Kool J.T.W., Perera M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallow S.J., van Aken S.E., Riedmiller S.B., Feldlym T.V.,
 RA Cho J.K., Quackenbush U., Sedegah M., Snoddy A., Cummings L.M.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
 RA Van Lin L.H., Jase C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.,
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii."
 RT Nature 419:512-519(2002).

CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DDA whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL; AAE010086; EAA22673.1; --
 SQ SEQUENCE 1153 AA; 135640 MW; ACFCE2E7D3D180E1 CRC64;

Qy Query Match
 Best Local Similarity 31.9%; Score 60; DB 2; Length 1153;
 Matches 12; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Qy 4 EPVEDNCINFVAMKFI-----DNTLYPIADDDNTLESD 36
 DB 8 EPKXKNCISNFKIXNEMLMKFEVKNIKVLESD 40

RESULT 25
 ID 08I291 PRELIMINARY; PRT; 995 AA.

AC 08I291; 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Hypothetical protein.

GN ORFNames=PF10_0308;
 OS Plasmodium falciparum (Isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=36329;

RP SEQUENCE FROM N.A.
 RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
 RA Gardner M.J., Hall N., Fung B., White O., Bertin M., Hyman R.W.,
 RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
 RA Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Angioli S.,
 RA Perera M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,
 RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
 RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Frazer C.M., Bartell B.,
 RT "Genome sequence of the human malaria parasite Plasmodium
 falciparum."
 RT Nature 419:498-511(2002).

DR EMBL; AE014834; AAN35505.1; --
 DR InterPro; IPR003323; OT0.
 DR Pfam; PF02338; OT0; 1.
 DR PROSITE; PS50802; OT0; 1.

KM Hypothetical protein.
 SQ SEQUENCE 995 AA; 118995 MW; C691E7E47DB52B30 CRC64;

Qy Query Match
 Best Local Similarity 30.3%; Score 57; DB 2; Length 995;
 Matches 12; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

CC Sigmoclon.
 CC NCBI_TaxID=42415;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed:14980081; DOI=10.1089/107999004772719873;
 RA Blanco J.C., Plezneva L., Boukhalova M., Richardson J.Y.,
 RT Harris K.A., Prince G.A.;
 RT "The cotton rat: an underutilized animal model for human infectious
 diseases can now be exploited using specific reagents to cytokines,
 chemokines, and interferons."
 RT J. Interferon Cytokine Res. 24:21-28(2004).
 RL EMBL; AY059406; AAL26703.1;
 DR HSP; Q14116; 1J08.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005149; P:interleukin-1 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR SMART; SM00125; IL1; 1.
 SQ SEQUENCE 196 AA; 22545 MW; E27C5BDC397F951C CRC64;
 Query Match 58.5%; Score 110; DB 2; Length 196;
 Best Local Similarity 63.9%; Pred. No. 1.6e-07;
 Matches 23; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 MAAPVEDNCINFAVAMKFIIDNTLYFIASDDEULESD 36
 Db 2 IAAPEEGSCIFRMTIDNTLYFIPEDNGBLESD 37
 RESULT 21
 ID IL18 RAT STANDARD; PRT; 194 AA.
 AC P97636; O88749; P97637;
 DT 15-JUL-1998 (Rel. 36; Created)
 DT 15-JUL-1998 (Rel. 36; Last sequence update)
 DT 25-OCT-2004 (Rel. 45; Last annotation update)
 DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
 DE (IRN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
 GN Name=IL18; Synonyms=Igf1;
 OS Rattus norvegicus (Rat);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
 RC STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
 RX MEDLINE=97152963; PubMed=8999896; DOI=10.1074/jbc.272.4.2035;
 RA Conti B., Jahng J.W., Tinct C., Son J.H., Joh T.H.;
 RT "Induction of interferon-gamma inducing factor in the adrenal
 cortex."
 RT J. Biol. Chem. 272:2035-2037(1997).
 RL J. Biol. Chem. 272:2035-2037(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=98368130; PubMed=9702748;
 RA Culhane A.C., Hall M.D., Rothwell N.J., Lusheshi G.N.;
 RT "Cloning of rat brain interleukin-18 cDNA."
 RT Mol. Psychiatry 3:362-366(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RC STRAIN=New England Deaconess Hospital; TISSUE=Adrenal gland;
 RA Kim S.-J., Kim C.-S., Song K.-Y., Kim U.-S., Jung K.-S.;
 RT "Cloning of the cDNA for interleukin-18 in PC12 and expression in
 Escherichia coli."
 RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Augments natural killer cell activity in spleen cells
 and stimulates interferon gamma production in T helper type 1
 cells.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Beta;
 CC IsoId=P97636-1; Sequence=Displayed;
 CC Name=Alpha;

CC IsoId=P97636-2; Sequence=VSP 002659;
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
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CC EMBL; U77776; AAC53009.1; -
 CC EMBL; U77777; AAC53010.1; -
 CC EMBL; AJ222813; CAA11001.1; -
 CC EMBL; AY258448; AAP14669.1; -
 CC RGD; 2889; 1118.
 DR GO; GO:0005576; C:extracellular; ISS.
 DR GO; GO:0005125; P:Cytokine activity; ISS.
 DR GO; GO:0001525; P:angiogenesis; ISS.
 DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; ISS.
 DR GO; GO:0042095; P:interferon-gamma biosynthesis; ISS.
 DR GO; GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.
 DR GO; GO:0030155; P:regulation of cell adhesion; ISS.
 DR GO; GO:0045188; P:regulation of circadian sleep/wake cycle, n. .; TBS.
 DR GO; GO:0030431; P:sleep; IDA.
 DR InterPro; IPR008996; Cytok IL1 like.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR SMART; SM00125; IL1; 1.
 KM Alternative splicing; Cytokine.
 FT PROPEP 1 36 By similarity.
 FT CHAIN 37 194 Interleukin-18.
 FT VARSPPLIC 121 139 Missing (in isoform Alpha).
 FT COMPLECT 4 5 MS -> IP (in Ref. 2).
 FT CONFLICT 48 48 I -> M (in Ref. 2).
 SQ SEQUENCE 194 AA; 22503 MW; E2089AD5F1798450 CRC64;
 Query Match 58.0%; Score 109; DB 1; Length 194;
 Best Local Similarity 61.1%; Pred. No. 2.2e-07;
 Matches 22; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 MAAPVEDNCINFAVAMKFIIDNTLYFIASDDEULESD 36
 Db 1 MAAPSEEGSCVFMFMFIIDNTLYFIPEDNGBLESD 36
 RESULT 22
 ID Q9MZL8 PRELIMINARY; PRT; 178 AA.
 AC Q9MZL8;
 DT 01-OCT-2000 (TrEMBL;rel. 15; Created)
 DT 01-OCT-2000 (TrEMBL;rel. 15; Last sequence update)
 DT 01-OCT-2003 (TrEMBL;rel. 25; Last annotation update)
 DE Interleukin-18 (Fragment).
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Olsen S.C., Lee I.K., Mwangi S.M., Kehli M., Bolin C.A.;
 RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RX EMBL; AF173175; AAF89833.1; -
 DR HSP; Q14116; 1J08.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005149; P:interleukin-1 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR008996; Cytok IL1 like.
 DR InterPro; IPR000975; Interleukin_1.
 DR SMART; SM00125; IL1; 1.

AC P70380, (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
 DB (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma)
 GN Name=1118; Synonyms=191f;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=96061009; PubMed=7477296; DOI=10.1038/378088a0;
 RA Okamura H., Taniuchi H., Komatsu T., Yutendo M., Hakura A., Tanimoto T.,
 RA Torigoe K., Okura T., Nukada Y., Hattori K., Akita K., Namba M.,
 RA Tanabe F., Konishi K., Fukuda S., Kurimoto M.,
 RT "Cloning of a new cytokine that induces IFN-gamma production by T
 RT cells."
 RL Nature 378:88-91 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshitsuki S., Carninci P., Prange C.,
 RA Raba S.S., Loguigno N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schell J.B., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP SEQUENCE OF 1-191 FROM N.A.
 RC STRAIN=NOD; TISSUE=Pancreas;
 RX MEDLINE=97174346; PubMed=9022080;
 RA Roche H., Jenkins N.A., Copeland N.G., Kolb H.,
 RT "Active stage of autoimmune diabetes is associated with the expression
 RT of a novel cytokine, IGIF, which is located near Id4."
 RL J. Clin. Invest. 99:469-474 (1997).
 CC -1- FUNCTION: Augments natural killer cell activity in spleen cells
 CC and stimulates interferon gamma production in T helper type I
 CC cells.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
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 CC -----
 DR EMBL; D49949; BAA08705.1; -
 DR EMBL; BC043844; AA043844.1; -
 DR EMBL; U66344; AB049753.1; -
 DR PIR; S60226; S60226.
 DR MGI; MGI:107936; 1118.
 DR GO; GO:0005576; C:extracellular; ISS.

DR GO; GO:0005125; P:cytokine activity; ISS.
 DR GO; GO:0001525; P:angiogenesis; ISS.
 DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
 DR GO; GO:0042253; P:granulocyte macrophage colony-stimulating f. . .; ISS.
 DR GO; GO:0008625; P:induction of apoptosis via death domain rec. . .; TAS.
 DR GO; GO:0042095; P:interferon-gamma biosynthesis; IMP.
 DR GO; GO:0042231; P:interleukin-13 biosynthesis; TAS.
 DR GO; GO:0042104; P:interleukin-2 biosynthesis; ISS.
 DR GO; GO:0042104; P:positive regulation of activated T-cell pro. . .; ISS.
 DR GO; GO:0030155; P:regulation of cell adhesion; ISS.
 DR GO; GO:0030431; P:sleep; ISS.
 DR InterPro; IPR008996; Cytok IL1 like.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1_1.
 DR SMART; SM00125; IL1_1.
 KM Cytokine; Direct protein sequencing.
 FT PROPEP 1 35
 FT CHAIN 36 192 Interleukin-18.
 FT CONFLICT 183 185 MFT -> IS (in Ref. 3).
 SQ SEQUENCE 192 AA; 22135 MW; 8FED938473874D63 CRC64;
 Query Match 58.5%; Score 110; DB 1; Length 192;
 Best Local Similarity 66.7%; Pred. No. 1.5e-07;
 Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 7 EDNCINPVAMKFTDNTLYPIAEDDENLESD 36
 DB 6 EDSQVNFKEMFTDNTLYPIEENGDESD 35
 ID 06US06 PRELIMINARY; PRT; 192 AA.
 AC 06US06;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Interleukin 18.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss; TISSUE=Liver;
 RA Tan Y., Shi Y., Lin L., Pang Y., Xu S., Duan X.,
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY362457; AA063045.1; -
 DR GO; GO:0006955; P:immune response; TAS.
 DR InterPro; IPR008996; Cytok IL1 like.
 SQ SEQUENCE 192 AA; 22075 MW; 8FED9399D0C24491 CRC64;
 Query Match 58.5%; Score 110; DB 2; Length 192;
 Best Local Similarity 66.7%; Pred. No. 1.5e-07;
 Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 7 EDNCINPVAMKFTDNTLYPIAEDDENLESD 36
 DB 6 EDSQVNFKEMFTDNTLYPIEENGDESD 35
 ID 091266 PRELIMINARY; PRT; 196 AA.
 AC 091266;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Interleukin 18.
 GN Name=1118;
 OS Sigmodon hispidus (Hispid cotton rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;

QY 1 MAAPVEDNCINFAVKFIDNTLYFIABDDENLESD 36
 DB 1 MAAPVEDNCINFAVKFIDNTLYFIABDDENLESD 36
 RESULT 15
 IL18 CANFA STANDARD; PRT; 193 AA.
 AC 09XSR01.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 03-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
 DE (Interleukin-18 precursor (IL-18) (Interleukin-1 gamma) (IL-1 gamma)).
 GN Name=IL18; Synonyms=IGIF;
 OS Carls family (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Falsipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99309818; PubMed=10380699; DOI=10.1007/s002510050532;
 RA Argyile D.J., McGillicvery C., Nicolson L., Orlows D.E.;
 RT "Cloning, sequencing, and characterization of dog interleukin-18."
 RL Immunogenetics 49:541-543(1999).
 CC -1- FUNCTION: Augments natural killer cell activity in spleen cells
 CC and stimulates interferon gamma production in T helper type 1
 CC cells (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
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 CC -----
 CC EMBL; Y11133; CA72015.1;
 DR GO; GO:0005576; C:extracellular; TAS.
 DR GO; GO:0005125; F:cytokine activity; TAS.
 DR GO; GO:0042033; P:chemokine biosynthesis; TAS.
 DR GO; GO:0008625; P:induction of apoptosis via death domain rec.; IEP.
 DR GO; GO:0042095; P:interferon-gamma biosynthesis; IDA.
 DR GO; GO:0042104; P:positive regulation of activated T-cell pro.; ISS.
 DR InterPro; IPR008996; Cytok_IL1_IL1ke.
 KM Cytokine.
 FT PROPEP 1 36 By similarity.
 FT CHAIN 37 193 Interleukin-18.
 SQ SEQUENCE 193 AA; 22037 MW; 0D973E586F461F25 CRC64;
 Query Match 72.3%; Score 136; DB 1; Length 193;
 Best Local Similarity 72.2%; Pred. No. 2.8e-11;
 Matches 26; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MAAPVEDNCINFAVKFIDNTLYFIABDDENLESD 36
 DB 1 MAAPVEDNCINFAVKFIDNTLYFIABDDENLESD 36
 RESULT 16
 Q80Y07 PRELIMINARY; PRT; 195 AA.
 AC Q80Y07.
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Interleukin 18.
 GN Name=IL18;
 OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
 OC

OC Meriones.
 OX NCBI_TaxID=10047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peritoneum;
 RX MEDLINE=22593022; PubMed=12706898; DOI=10.1016/S0378-1119(03)00457-8;
 RA Gaucher D., Chadee K.;
 RT "Gerbil interleukin-18 and caspase-1: cloning, expression and
 RT characterization."
 RL Gene 307:159-166(2003).
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 DR EMBL; AY095932; AA03434.1;
 DR HSSP; Q14116; 100S.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR008996; Cytok_IL1_IL1ke.
 DR InterPro; IPR009975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR SMART; SM00125; IL1; 1.
 SQ SEQUENCE 195 AA; 22172 MW; C6F815317953154D CRC64;
 Query Match 64.4%; Score 121; DB 2; Length 195;
 Best Local Similarity 66.7%; Pred. No. 4.1e-09;
 Matches 24; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MAAPVEDNCINFAVKFIDNTLYFIABDDENLESD 36
 DB 2 MAAPVEDNCINFAVKFIDNTLYFIABDDENLESD 37
 RESULT 17
 Q80S88 PRELIMINARY; PRT; 189 AA.
 AC Q80S88.
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Interleukin 18.
 GN Name=IL18;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B10.S/DvTe, and SUI/0; TISSUE=Spleen;
 RA Gao J., Teuscher C.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 DR EMBL; AY157834; AA021309.1;
 DR HSSP; AY157835; AA021310.1;
 DR HSSP; Q14116; 100S.
 DR MGD; MGI:107936; IL18.
 DR GO; GO:0006955; P:immune response; TAS.
 DR InterPro; IPR008996; Cytok_IL1_IL1ke.
 DR InterPro; IPR009975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR SMART; SM00125; IL1; 1.
 SQ SEQUENCE 189 AA; 21862 MW; E8F9E5EC0186465 CRC64;
 Query Match 58.5%; Score 110; DB 2; Length 189;
 Best Local Similarity 66.7%; Pred. No. 1.5e-07;
 Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 7 EDNCINFAVKFIDNTLYFIABDDENLESD 36
 DB 3 EDNCINFAVKFIDNTLYFIABDDENLESD 32
 RESULT 18
 IL18 MOUSE STANDARD; PRT; 192 AA.
 ID IL18_MOUSE

```

QY 1 MAEPVEDNCINPVAMKFIIDNTLYFAEDDENLESD 36
DB 1 MAEPV-DNCISFVEMKFIINTLYFAVENDDELESD 35

RESULT 11
IL18_BOVIN STANDARD; PRT; 193 AA.
AC 09T073;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
GN Name=IL18;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
NCBI_TaxID=9913;
RX MEDLINE=20012648; PubMed=10547157; DOI=10.1089/1079990933118;
RA Shoda L.K., Zarlega D.S., Hirano A., Brown W.C.; and analysis of IL-
RT "Cloning of a cDNA encoding bovine Interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity."
RT J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -1- FUNCTION: Augments natural killer cell activity in spleen cells
CC and stimulates interferon gamma production in T helper type I
CC cells (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AF124789; AAP08686.1; -
DR InterPro; IPR008996; CytoK_IL1_1like.
DR SMART; SM00125; IL1; 1.
DR CYCBase.
KW PROPEP.
FT CHAIN 1 36 By similarity.
FT INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match
Best Local Similarity 77.7%; Score 146; DB 1; Length 193;
Matches 28; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAEPVEDNCINPVAMKFIIDNTLYFAEDDENLESD 36
DB 1 MAEPVEDNCISFVEMKFIINTLYFAVENDDELESD 36

RESULT 12
O6TLW4 PRELIMINARY; PRT; 193 AA.
AC 06TLW4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Interleukin 18.
GN Name=IL18;
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bubalus.
NCBI_TaxID=89462;
SQ SEQUENCE 193 AA; 22190 MW; 93103B5C62B745DB CRC64;

Query Match
Best Local Similarity 75.5%; Score 142; DB 2; Length 193;
Matches 27; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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RN (1)
RP SEQUENCE FROM N.A.
RA Chaudhuri P., Bera B.C.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY394479; AAQ94552.1; -
DR InterPro; IPR008996; CytoK_IL1_1like.
SQ SEQUENCE 193 AA; 22176 MW; 66116F198DE94BC4 CRC64;

Query Match
Best Local Similarity 77.7%; Score 146; DB 2; Length 193;
Matches 28; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAEPVEDNCINPVAMKFIIDNTLYFAEDDENLESD 36
DB 1 MAEPVEDNCISFVEMKFIINTLYFAVENDDELESD 36

RESULT 13
O95M33 PRELIMINARY; PRT; 192 AA.
AC 095M33;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Interferon-gamma inducing factor.
GN Name=IGIF;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID=9685;
RX MEDLINE=10547157; PubMed=10547157; DOI=10.1089/1079990933118;
RA Shoda L.K., Zarlega D.S., Hirano A., Brown W.C.; and analysis of IL-
RT "Cloning of a cDNA encoding bovine Interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity."
RT J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -1- FUNCTION: Augments natural killer cell activity in spleen cells
CC and stimulates interferon gamma production in T helper type I
CC cells (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AF124789; AAP08686.1; -
DR InterPro; IPR008996; CytoK_IL1_1like.
DR SMART; SM00125; IL1; 1.
DR CYCBase.
KW PROPEP.
FT CHAIN 1 36 By similarity.
FT INTERLEUKIN-18.
SQ SEQUENCE 192 AA; 22068 MW; 5878CD3DAC7A43358 CRC64;

Query Match
Best Local Similarity 76.3%; Score 143.5; DB 2; Length 192;
Matches 28; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 1 MAEPVEDNCINPVAMKFIIDNTLYFAEDDENLESD 36
DB 1 MAEPVEDNCISFVEMKFIINTLYFAVENDDELESD 35

RESULT 14
O6T573 PRELIMINARY; PRT; 193 AA.
AC 06T573;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Interleukin-18.
GN Name=IL18;
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bubalus.
NCBI_TaxID=89462;
RX MEDLINE=10547157; PubMed=10547157; DOI=10.1089/1079990933118;
RA Shoda L.K., Zarlega D.S., Hirano A., Brown W.C.; and analysis of IL-
RT "Cloning of a cDNA encoding bovine Interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity."
RT J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -1- FUNCTION: Augments natural killer cell activity in spleen cells
CC and stimulates interferon gamma production in T helper type I
CC cells (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AF124789; AAP08686.1; -
DR InterPro; IPR008996; CytoK_IL1_1like.
DR SMART; SM00125; IL1; 1.
DR CYCBase.
KW PROPEP.
FT CHAIN 1 36 By similarity.
FT INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22190 MW; 93103B5C62B745DB CRC64;

Query Match
Best Local Similarity 75.5%; Score 142; DB 2; Length 193;
Matches 27; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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DB 1 MAABVED-CINPVEKFIINTLYFVADNDESD 35

RESULT 8
ID IL18_PIG STANDARD; PRT; 192 AA.
AC 019073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
GN (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
OS Name-IL18; Synonym-IGIF;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN 1;
RP SEQUENCE FROM N.A.
RA Foss D.L., Murtough M.P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN 2;
RP SEQUENCE FROM N.A.
RA Penha-Goncalves M.N., Logan N.A., Nicolson L., Onions D.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN 3;
RP SEQUENCE FROM N.A.
RA Muneta Y., Mori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN 4;
RP TISSUE=Intestine;
RX MEDLINE=20260994; PubMed=10803849; DOI=10.1007/s002510050630;
RA Fourtout S., Dozolis C.M., Yerie M., Pincon P., Faltbrother J.M.,
RA Oswald B., Oswald I.P.;
RT "Cloning, chromosomal location, and tissue expression of the gene for
RT p15 Interleukin-18";
RL Immunogenetics 51:358-365(2000).
CC -1- FUNCTION: Augments natural killer cell activity in spleen cells
CC and stimulates interferon gamma production in T helper type 1
CC cells (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-1 family.
CC -----
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CC -----
DR EMBL; U68701; AAC18415.1; -
DR EMBL; Y11132; CA272014.1; -
DR EMBL; AB010003; BAA24135.1; -
DR EMBL; AF191088; AAF71200.1; -
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005125; P:cytokine activity; IMP.
DR GO; GO:0001525; P:angiogenesis; ISS.
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec.; IDA.
DR GO; GO:0042035; P:interferon-gamma biosynthesis; IDA.
DR GO; GO:0042104; P:positive regulation of activated T-cell pro.; ISS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
DR CYTOKINE.
KM CYTOKINE.
FT PROPEP 1 35 By similarity.
FT CHAIN 36 192 Interleukin-18.
SQ SEQUENCE 192 AA; 22026 MW; 881E654E221A17A CRC64;

Query Match 78.5%; Score 147.5; DB 1; Length 192;
Best Local Similarity 80.6%; Pred. No. 6.1e-13;
Matches 29; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 MAABVED-CINPVEKFIINTLYFVADNDESD 36
DB 1 MAABP-EDNCISFVEMKFIINTLYFVADNDESD 35

RESULT 9
ID Q9NIP7 PRELIMINARY; PRT; 192 AA.
AC Q9NIP7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Interleukin-18.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20356335; PubMed=10901174;
RA Oem J.K., Song H.J., Kang S.W., Jeong W.S.;
RT "Cloning, sequencing, and expression of porcine interleukin-18 in
RT Escherichia coli";
RL Mol. Cells 10:343-347(2000).
DR EMBL; AF176949; AAF35169.1; -
DR HSBP; Q14116; I005.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; P:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 192 AA; 21969 MW; A51EB7A4E221A16D CRC64;

Query Match 78.5%; Score 147.5; DB 2; Length 192;
Best Local Similarity 80.6%; Pred. No. 6.1e-13;
Matches 29; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 MAABVED-CINPVEKFIINTLYFVADNDESD 36
DB 1 MAABP-EDNCISFVEMKFIINTLYFVADNDESD 35

RESULT 10
ID Q6STL7 PRELIMINARY; PRT; 177 AA.
AC Q6STL7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Interleukin 18.
GN Name-IL-18;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN 1;
RP SEQUENCE FROM N.A.
RA Lu X., Hui L.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY50287; AAR27432.1; -
DR InterPro; IPR008996; Cytok IL1 like.
SQ SEQUENCE 177 AA; 20300 MW; 426F30330EB1F815 CRC64;

Query Match 77.9%; Score 146.5; DB 2; Length 177;
Best Local Similarity 80.6%; Pred. No. 7.8e-13;
Matches 29; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

AC 09X807;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
 DB (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
 GN Name=IL18; Synonyms=IGIF;
 OS Equus caballus (Horse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nicolson L., Pena-Gonzales M.N., Keanie J.L., Logan N.A.,
 RA Artye D.J., Orlons D.E.;
 RT Nucleotide sequence of equine interleukin 12 and 18 cDNAs."
 RL Submitted (FE8-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Augments natural killer cell activity in spleen cells
 CC and stimulates interferon gamma production in T helper type 1
 CC cells (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
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 CC -----
 CC EMBL: Y1131; CAA72013.1;
 DR InterPro: IPR008996; Cyclo_IL1_1like.
 KW Cyclokin.
 FT PROPEP 1 36 By similarity.
 FT CHAIN 37 193 Interleukin-18.
 SQ SEQUENCE 193 AA; 22058 MW; 4D81535E9004EBCF CRC64;
 QY Query Match 84.6%; Score 159; DB 1; Length 193;
 Best Local Similarity 83.3%; Pred. No. 1,4e-14;
 Matches 30; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 DB 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 36
 1 MAAGPVEDNCISLVEMKFIIDNTLYFAEDDENLESD 36
 QY
 DB
 RESULT 5
 ID 06WUJ7 PRELIMINARY; PRT; 189 AA.
 AC 06WUJ7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE DELTA3-PRO-IL-18.
 GN Name=IL18;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gaggero A., De Ambrosio A., Mezzananza D., Piazza T., Rubartelli A.,
 RA Fagiani M., Canevari S., Parrini S.;
 RT A novel isoform of pro-interleukin-18 expressed in ovarian tumors is
 RT resistant to caspase-1 and -4 processing."
 RL Oncogene 0:0-0(2004).
 DR EMBL: AY266351; AAP2312.1;
 DR InterPro: IPR008996; Cyclo_IL1_1like.
 SQ SEQUENCE 189 AA; 21896 MW; A8BA275CF73JA4B6 CRC64;
 QY Query Match 82.4%; Score 155; DB 2; Length 189;
 Best Local Similarity 88.9%; Pred. No. 5e-14;

Matches 32; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 QY 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 36
 DB 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 32
 QY
 DB
 RESULT 6
 ID 09GL09 PRELIMINARY; PRT; 193 AA.
 AC 09GL09;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Interleukin-18 (IGIF).
 GN Name=IL-18;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bailey S.L., Gosner A., Dalziel R., Hopkins J.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF401033; CAC09326.2; -.
 DR HSSP: Q1416; 1J08.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005149; F:interleukin-1 receptor binding; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR008996; Cyclo_IL1_1like.
 DR InterPro: IPR000975; Interleukin_1.
 DR SMART: SM00125; IL1_1.
 SQ SEQUENCE 193 AA; 22166 MW; CCDOA329062EP18C CRC64;
 QY Query Match 82.4%; Score 155; DB 2; Length 193;
 Best Local Similarity 80.6%; Pred. No. 5.1e-14;
 Matches 29; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 36
 DB 1 MAAPVEDNCISLVEMKFIIDNTLYFAEDDENLESD 36
 QY
 DB
 RESULT 7
 ID 085B8 PRELIMINARY; PRT; 192 AA.
 AC 085B8;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Interferon gamma inducing factor precursor.
 GN Name=IFI-18;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kawanara C., Kawakami K., Kishi M., Mochizuki M.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB056857; BAC65243.1; -.
 DR HSSP: Q1416; 1J08.
 DR InterPro: IPR008996; Cyclo_IL1_1like.
 KW Signal.
 FT SIGNAL 1 35 Potential.
 SQ SEQUENCE 192 AA; 22071 MW; 204F32D131588513 CRC64;
 QY Query Match 82.2%; Score 154.5; DB 2; Length 192;
 Best Local Similarity 83.3%; Pred. No. 6e-14;
 Matches 30; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
 QY 1 MAAPVEDNCINFVAMKFIIDNTLYFAEDDENLESD 36

RA Butterfield V.S.N., Krzywnicki M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN (5)
 RP SEQUENCE OF 2-193 FROM N.A.
 RC TISSUE-Peripheral blood.
 RA Contt B., Kim S.J., Tint C., Chun H.S., Joh T.H.,
 RA Submitted (Feb-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Augments natural killer cell activity in spleen cells
 CC and stimulates interferon gamma production in T helper type 1
 CC cells.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL; D49950; BAA08706.1; -
 DR EMBL; AF077611; AAC37787.1; -
 DR EMBL; AY044641; AAK5950.1; -
 DR EMBL; BC007007; AAH07007.1; -
 DR EMBL; BC007461; AAH07461.1; -
 DR EMBL; U90434; AAB50010.1; -
 DR PDB; 1J0S; NMR; A=37-193.
 DR OGP; Q14116; -
 DR GeneW; HGNC:5986; IL18.
 DR H-InvDB; HIX0010123; -
 DR MIM; 600953; -
 DR GO; GO:0005576; C:extracellular; TAS.
 DR GO; GO:0005125; F:cytokine activity; TAS.
 DR GO; GO:0004871; F:signal transducer activity; TAS.
 DR GO; GO:0001525; P:angiogenesis; IDA.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0042033; P:chemokine biosynthesis; TAS.
 DR GO; GO:0042253; P:granulocyte macrophage colony-stimulating f...; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR GO; GO:0008635; P:induction of apoptosis via death domain rec...; ISS.
 DR GO; GO:0042035; P:interferon-gamma biosynthesis; TAS.
 DR GO; GO:0042231; P:interleukin-13 biosynthesis; TAS.
 DR GO; GO:0042094; P:interleukin-2 biosynthesis; TAS.
 DR GO; GO:0042104; P:positive regulation of activated T-cell pro...; IDA.
 DR GO; GO:0030155; P:regulation of cell adhesion; IDA.
 DR GO; GO:0030431; P:sleep; ISS.
 DR GO; GO:0042092; P:T-helper 2 type immune response; TAS.
 DR InterPro; IPR008996; Cytok_IL11ike.
 DR SMART; SM00125; IL1; 1.
 DR 3D-structure; Cytokine.
 FT PROPEP 1 36 By similarity.
 FT CHAIN 37 193 Interleukin-18.
 FT CONFLICT 66 66 F -> L (in Ref. 2).
 FT CONFLICT 86 86 S -> R (in Ref. 2).
 FT CONFLICT 191 191 N -> S (in Ref. 2).
 SQ SEQUENCE 193 AA; 22326 MW; 323C62C20378BD55 CRC64;

Query Match 100.0%; Score 188; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 9.2e-19;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAAPVEDNCINPAMKFIIDNTLYFAEDDENLESD 36
 1 MAAPVEDNCINPAMKFIIDNTLYFAEDDENLESD 36

RESULT 2
 096KJ8

ID 096KJ8 PRELIMINARY; PRT; 193 AA.
 AC 096KJ8;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Interleukin 18.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ying P., Jianxin L.;
 RA Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF380360; AAK57024.1; -
 DR HSSP; Q14116; 1J0S.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR008996; Cytok_IL11ike.
 DR InterPro; IPR000975; Interleukin_1.
 DR SMART; SM00125; IL1; 1.
 SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match 100.0%; Score 188; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 9.2e-19;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAAPVEDNCINPAMKFIIDNTLYFAEDDENLESD 36
 1 MAAPVEDNCINPAMKFIIDNTLYFAEDDENLESD 36

RESULT 3

ID 096G15 PRELIMINARY; PRT; 193 AA.
 AC 096G15;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Interleukin-18.
 GN Name=IL18;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_Taxid=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=2129850; PubMed=11331040; DOI=10.1089/107999001750133212;
 RA Glavetov L.D., Imhoof J.D., Parodi L.M., Velasquillo C.M.,
 RA Hodara V.L.;
 RT "Expression of the interleukin-18 gene from rhesus macaque by the
 RT simian immunodeficiency virus does not result in increased viral
 RT replication." J. Interferon Cytokine Res. 21:173-180 (2001).
 RL J. Interferon Cytokine Res. 21:173-180 (2001).
 DR EMBL; AF303732; AAK13416.1; -
 DR HSSP; Q14116; 1J0S.
 DR InterPro; IPR008996; Cytok_IL11ike.
 SQ SEQUENCE 193 AA; 22325 MW; B2BD29C03BB05E CRC64;

Query Match 95.2%; Score 179; DB 2; Length 193;
 Best Local Similarity 94.4%; Pred. No. 1.8e-17;
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MAAPVEDNCINPAMKFIIDNTLYFAEDDENLESD 36
 1 MAAPVEDNCINPAMKFIIDNTLYFAEDDENLESD 36

RESULT 4
 IL18_HORSE STANDARD; PRT; 193 AA.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2005, 12:15:40 / Search time 175 Seconds
(without alignments)
105.342 Million cell updates/sec

Title: US-09-711-896a-1

Perfect score: 188
Sequence: 1 NAAPEVDNCINFAKPFIDNTLYFAEDDENLESD 36

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: 1: uniprot_sprot;
2: uniprot_trembl;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	188	100.0	193 1 IL18 HUMAN	Q14116 homo sapien
2	188	100.0	193 2 Q96KJ8	Q96KJ8 homo sapien
3	179	95.2	193 2 Q9BG15	Q9BG15 macaca mula
4	159	84.6	193 1 IL18 HORSE	Q9X877 equus caball
5	155	82.4	189 2 Q6WJ7	Q6WJ7 homo sapien
6	155	82.4	193 2 Q9GL09	Q9GL09 civis aries
7	154.5	82.2	192 2 Q865B8	Q865B8 felis silve
8	147.5	78.5	192 1 IL18 PIG	Q19073 sus scrofa
9	147.5	78.5	192 2 Q9N1F7	Q9N1F7 sus scrofa
10	146.5	77.9	177 2 Q8STL7	Q8STL7 sus scrofa
11	146	77.7	193 1 IL18 BOVIN	Q9TUV3 bos taurus
12	146	77.7	193 2 Q6TLM4	Q6TLM4 bubalus bub
13	143.5	76.3	192 2 Q9SM33	Q9SM33 felis silve
14	142	75.5	193 2 Q6T573	Q6T573 bubalus bub
15	136	72.3	193 1 IL18 CANFA	Q9X870 canis fami
16	121	64.4	195 2 Q80707	Q80707 meriones un
17	110	58.5	189 2 Q80S88	Q80S88 mus musculu
18	110	58.5	192 1 IL18 MOUSE	P70388 mus musculu
19	110	58.5	192 2 Q6USQ6	Q6USQ6 mus musculu
20	110	58.5	196 2 Q91Z66	Q91Z66 sigmodon hi
21	109	58.0	194 1 IL18 RAT	P97656 rattus norv
22	93	49.5	178 2 Q9WZL8	Q9WZL8 bos taurus
23	62.5	33.2	1643 2 Q96Z44	Q96Z44 plasmodium
24	60	31.9	1163 2 Q7RWJ4	Q7RWJ4 plasmodium
25	57	30.3	2 Q81J91	Q81J91 plasmodium
26	56	29.8	1106 2 Q87J35	Q87J35 neurospora
27	55	29.3	2 Q997R3	Q997R3 staphylococ
28	55	29.3	2 Q7A017	Q7A017 staphylococ
29	55	29.3	2 Q7A513	Q7A513 staphylococ
30	55	29.3	2 Q6G843	Q6G843 staphylococ
31	55	29.3	2 Q6GFT8	Q6GFT8 staphylococ

32	55	29.3	688 1 CACM YEAST	P80235 saccharomyc
33	55	29.3	862 2 Q6CUT7	Q6CUT7 kluyveromyc
34	54.5	29.0	439 2 Q7Q5F7	Q7Q5F7 anopheles g
35	54	28.7	417 2 Q96410	Q96410 hydra attenu
36	54	28.7	921 2 Q7YZ56	Q7YZ56 cryptospori
37	53.5	28.5	494 2 Q86A22	Q86A22 dictyostell
38	53.5	28.5	1055 2 Q6S146	Q6S146 african swi
39	53	28.2	70 2 Q9JN03	Q9JN03 campylobact
40	53	28.2	99 2 Q776W7	Q776W7 bacteriophag
41	53	28.2	298 2 Q858S2	Q858S2 bacteriophag
42	53	28.2	365 2 Q9PNP3	Q9PNP3 campylobact
43	53	28.2	956 2 Q7RG03	Q7RG03 plasmodium
44	53	28.2	1039 2 Q9CV97	Q9CV97 toxoplasma
45	52.5	27.9	130 2 Q6MKQ3	Q6MKQ3 bdellovibri

ALIGNMENTS

RESULT 1	IL18 HUMAN	STANDARD;	PRT;	193 AA.
AC	Q14116, Q75599,			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)			
DE	(ILFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).			
GN	Name=IL18; Synonyms=IGIF			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=96247646; PubMed=8666798;			
RA	Ushio S., Namba M., Okura T., Hattori K., Mukada Y., Akita K.,			
RA	Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,			
RA	Fukuda S., Ikeda M., Okamura H., Kurimoto M.;			
RT	"Cloning of the cDNA for human IFN-gamma-inducing factor, expression			
RT	in Escherichia coli, and studies on the biologic activities of the			
RT	protein.";			
RL	J. Immunol. 156:4274-4279 (1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Tong D., Guixin D., Lihua H., Haitao W.;			
RT	"Cloning and sequencing of the cDNA for precursor hIL-18.";			
RT	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Liu J., Peng X., Yuan J., Qiang B.;			
RT	"Cloning of human interleukin 18 cDNA.";			
RT	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Urinary bladder;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899.			
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schaller G.D.,			
RA	Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Scapleton M., Soares M.B., Bonaldo M.B., Casavant J.L., Scheetz T.E.,			
RA	Brownstein M.U., Ueda T.B., Toshiyuki S., Carninci P., Zhang C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Peterson R.D., Millar S.J.,			
RA	Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Valley D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley M., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			

PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: US 60/230,610
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: US 60/230,597
 PRIOR FILING DATE: 2000-09-06
 Remaining Prior Application data removed - See file wrapper or PALM.
 NUMBER OF SEQ ID NOS: 506
 SOFTWARE: PERL Program
 SEQ ID NO 363
 LENGTH: 185
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc.feature
 OTHER INFORMATION: incyle ID NO: LG:1015157.1.orfl:2000SEP08
 US-10-363-616-488

Query Match 26.3%; Score 49.5; DB 15; Length 185;
 Best Local Similarity 45.5%; Pred. No. 65;
 Matches 10; Conservative 7; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVAMKFIIDNTLYFIADDDEN 32
 DB 62 LDFPSMKF---SLYFLAYEDKN 80

RESULT 39
 US-10-369-493-13822
 Sequence 13822, Application US/10369493
 Publication No: US20030233675A1
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfang
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 13822
 LENGTH: 380
 TYPE: PRT
 ORGANISM: Pseudomonas fluorescens
 US-10-369-493-13822

Query Match 26.3%; Score 49.5; DB 15; Length 380;
 Best Local Similarity 37.5%; Pred. No. 1.5e+02;
 Matches 12; Conservative 3; Mismatches 16; Indels 1; Gaps 1;

QY 2 AAEFVEDNCINFVAMKFIIDNTLYFIADDDEN 33
 DB 205 AANPITDACA-LKAMTLISNNLRVVDGSDL 235

RESULT 40
 US-10-363-616-488
 Sequence 488, Application US/10363616
 Publication No: US20040044181A1
 GENERAL INFORMATION:
 APPLICANT: Hygeeq, Inc
 TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
 FILE REFERENCE: 21272-113 (793)
 CURRENT APPLICATION NUMBER: US/10/363,616
 CURRENT FILING DATE: 2003-03-03
 PRIOR APPLICATION NUMBER: 09/654,935
 PRIOR FILING DATE: 2000-09-01
 NUMBER OF SEQ ID NOS: 490
 SEQ ID NO 488

LENGTH: 547
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-363-616-488

Query Match 26.3%; Score 49.5; DB 15; Length 547;
 Best Local Similarity 39.4%; Pred. No. 2.3e+02;
 Matches 13; Conservative 5; Mismatches 8; Indels 7; Gaps 2;

QY 7 EDNCINFVAMKFIIDNTLY---FIADDDENLESD 36
 DB 315 EDGCIIVDVIAVEDNSLYQLFYLA---NLNOD 343

Search completed: May 13, 2005, 12:38:10
 Job time : 135 secs

Db 308 ISSDPMEDVCCQOLYTRFISNTI 330

RESULT 35

US-10-087-167-14
Sequence 14, Application US/10087167
Publication No. US20030154509A1
GENERAL INFORMATION:
APPLICANT: Pascal, Erica
APPLICANT: Valentine, Scott
APPLICANT: Brown, Jeffrey
APPLICANT: Cockrell, Adam
APPLICANT: Johnson, Brian
TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
FILE REFERENCE: 50018A
CURRENT APPLICATION NUMBER: US/10/087,167
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/242,969
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 536
TYPE: PRT
ORGANISM: Chironomus tentans
US-10-087-167-14

Query Match 26.6%; Score 50; DB 14; Length 536;
Best Local Similarity 38.5%; Pred. No. 1.9e+02;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 11 INFVANKPFDNTLYFAEDDENLESD 36
Db 16 LNVASQSPGDNNITYGATKKQRLSESD 41

RESULT 36

US-10-606-060A-9
Sequence 9, Application US/10606060A
Publication No. US20040058369A1
GENERAL INFORMATION:
APPLICANT: Syngenta
APPLICANT: Jepsen, Ian
APPLICANT: Martinez, Alberto
APPLICANT: Greenland, Andrew James
TITLE OF INVENTION: A GENE SWITCH
FILE REFERENCE: 1392/4/3/2
CURRENT APPLICATION NUMBER: US/10/606,060A
CURRENT FILING DATE: 2003-06-25
PRIOR APPLICATION NUMBER: US 08/553,648
PRIOR FILING DATE: 1996-05-24
PRIOR APPLICATION NUMBER: US 09/564,418
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.2
SEQ ID NO 9
LENGTH: 536
TYPE: PRT
ORGANISM: Chironomus tentans
US-10-606-060A-9

Query Match 26.6%; Score 50; DB 15; Length 536;
Best Local Similarity 38.5%; Pred. No. 1.9e+02;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 11 INFVANKPFDNTLYFAEDDENLESD 36
Db 16 LNVASQSPGDNNITYGATKKQRLSESD 41

RESULT 37
US-10-437-963-141822

Sequence 141822, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yinhua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boulharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 141822
LENGTH: 663
TYPE: PRT
ORGANISM: Oryza sativa
FEATURES:
OTHER INFORMATION: Clone ID: PAT_MRT4530_4288C.1.pap
US-10-437-963-141822

Query Match 26.6%; Score 50; DB 16; Length 663;
Best Local Similarity 32.1%; Pred. No. 2.4e+02;
Matches 9; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 2 AAEPVEDNCINFVANKPFDNTLYFAED 29
Db 206 APEALSLNCVKSNGVNVDTGTYWLTED 233

RESULT 38

US-10-363-829-363
Sequence 363, Application US/10363829
Publication No. US20040142331A1
GENERAL INFORMATION:
APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
APPLICANT: Dahl, Christopher R.; Momiya, Monika G.;
APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
APPLICANT: Gerstl, Jr., Edward H.; Peralta, Careyna H.;
APPLICANT: David, Marie H.; Panzer, Scott R.;
APPLICANT: Flores, Vincent Z.; Daffo, Abel;
APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
APPLICANT: Chang, Simon C.; Au, Alan P.;
APPLICANT: Imman, Redekah R.
TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
FILE REFERENCE: PT-1183 USN
CURRENT APPLICATION NUMBER: US/10/363,829
CURRENT FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: PCT/US01/27628
PRIOR FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/229,751
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/229,749
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/229,750
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/229,747
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/229,748
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/230,583
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/230,517

US-10-437-963-150952
Sequence 150952, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bouharov, Andrey A.
APPLICANT: Bardazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 150952
LENGTH: 224
TYPE: PRT
ORGANISM: *Oryza sativa*
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(224)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_51140C.1.pcp
US-10-437-963-150952

Query Match 26.9%; Score 50.5; DB 16; Length 224;
Best Local Similarity 35.7%; Pred. No. 59;
Matches 10; Conservative 6; Mismatches 9; Indels 3; Gaps 1;

QY 5 PVEDNCINFVAMKFIIDNTLYPIAEDDEN 32
DB 135 PIEDLCIDPTLPFGPD---YIIXEGSEN 159

RESULT 32
US-10-437-963-150950
Sequence 150950, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bouharov, Andrey A.
APPLICANT: Bardazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 150950
LENGTH: 1083
TYPE: PRT
ORGANISM: *Oryza sativa*
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1083)
OTHER INFORMATION: Clone ID: PAT_MRT4530_51139C.1.pcp
US-10-437-963-150950

Query Match 26.9%; Score 50.5; DB 16; Length 1083;
Best Local Similarity 35.7%; Pred. No. 3.7e+02;
Matches 10; Conservative 6; Mismatches 9; Indels 3; Gaps 1;

QY 5 PVEDNCINFVAMKFIIDNTLYPIAEDDEN 32
DB 868 PIEDLCIDPTLPFGPD---YIIXEGSEN 892

RESULT 33
US-09-748-637A-318
Sequence 318, Application US/09749637A
Patent No. US20020173449A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Oliviera, Baldomero M.
APPLICANT: Carter, G. Edward
APPLICANT: Watkins, Warren
APPLICANT: Hilliard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Laver, Richard T.
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
FILE REFERENCE: 2314-227
CURRENT APPLICATION NUMBER: US/09/749,637A
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/243,412
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US60/219,440
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/214,263
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/173,754
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 409
SOFTWARE: Patent version 3.0
SEQ ID NO 318
LENGTH: 718
TYPE: PRT
ORGANISM: *Conus imperialis*
US-09-749-637A-318

Query Match 26.6%; Score 50; DB 9; Length 78;
Best Local Similarity 34.8%; Pred. No. 20;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 10 CINFVAMKFIIDNTLYPIAEDDEN 32
DB 5 CVFPAVAFELTASVFTADDSRN 27

RESULT 34
US-10-424-599-174564
Sequence 174564, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 174564
LENGTH: 438
TYPE: PRT
ORGANISM: *Glycine max*
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(438)
OTHER INFORMATION: Clone ID: PAT_MRT3847_12864C.1.pcp
US-10-424-599-174564

Query Match 26.6%; Score 50; DB 15; Length 438;
Best Local Similarity 34.8%; Pred. No. 1.5e+02;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAEPVEDNCINFVAMKFIIDNTL 23


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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33630
LENGTH: 156
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AP000241.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 2.9
OTHER INFORMATION: EST HUMAN HIT: A1652927.1, EVALU 9.00e-25
OTHER INFORMATION: EST HUMAN HIT: O14867, EVALU 2.00e-89
OTHER INFORMATION: EST HUMAN HIT: AUI34963.1, EVALU 1.00e-69
US-09-864-761-33630.

Query Match      27.7% Score 52; DB 9; Length 156;
Best Local Similarity 31.8% Pred. No. 24;
Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Cy 1 MAAPVEDNCGINPAMKFIQNT 22
Db 12 LSVHNIESCFQFLKFKFLDST 33

RESULT 27
US-09-864-761-46601
Sequence 46601, Application US/09864761
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Acoimca-X-1

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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 46601
LENGTH: 445
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AP000201.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
OTHER INFORMATION: EST HUMAN HIT: AUI34963.1, EVALU 1.00e-130
OTHER INFORMATION: EST HUMAN HIT: O14867, EVALU 0.00e+00
US-09-864-761-46601

Query Match      27.7% Score 52; DB 9; Length 445;
Best Local Similarity 31.8% Pred. No. 80;
Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Cy 1 MAAPVEDNCGINPAMKFIQNT 22
Db 35 LSVHNIESCFQFLKFKFLDST 56

RESULT 28
US-09-864-761-47605
Sequence 47605, Application US/09864761
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.

```

APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 1397
 LENGTH: 687
 TYPE: PRT
 ORGANISM: Saccharomyces cerevisiae
 US-10-369-493-1397

Query Match 29.3%; Score 55; DB 15; Length 687;
 Best Local Similarity 34.5%; Pred. No. 50;
 Matches 10; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 8 DNCINFVAMKFIIDNTLYFAEDDENLESD 36
 DB 260 DDCMKNKLDLSALFVCLDVAAPAD 288

RESULT 23
 US-10-872-874-158
 Sequence 158, Application US/10872874
 Publication No. US20050003419A1
 GENERAL INFORMATION:
 APPLICANT: Breves, Roland
 APPLICANT: Maurel, Karl-Heinz
 APPLICANT: Eck, Jurgen
 APPLICANT: Lorenz, Patrick
 APPLICANT: Zinke, Holger
 TITLE OF INVENTION: GLYCOSYL HYDROLASES
 FILE REFERENCE: HENK-0088 / H 5206
 CURRENT APPLICATION NUMBER: US/10/872,874
 CURRENT FILING DATE: 2004-06-21
 PRIOR APPLICATION NUMBER: PCT/EP02/14210
 PRIOR FILING DATE: 2002-12-13
 PRIOR APPLICATION NUMBER: DE 101 63 748.9
 PRIOR FILING DATE: 2001-12-21
 NUMBER OF SEQ ID NOS: 320
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 158
 LENGTH: 81
 TYPE: PRT
 ORGANISM: Streptomyces coelicolor
 US-10-872-874-158

Query Match 28.7%; Score 54; DB 16; Length 81;
 Best Local Similarity 43.5%; Pred. No. 5.8;
 Matches 10; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 14 VAMKFIIDNTLYFAEDDENLESD 36
 DB 20 VSLKSIDNTLYRLEEDKRFYTD 42

RESULT 24
 US-10-369-493-11186
 Sequence 1186, Application US/10369493
 Publication No. US20030233675A1
 GENERAL INFORMATION:
 APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 11186
 LENGTH: 679
 TYPE: PRT
 ORGANISM: Methanosarcina mazei
 US-10-369-493-11186

Query Match 28.2%; Score 53; DB 15; Length 679;
 Best Local Similarity 37.9%; Pred. No. 94;
 Matches 11; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 8 DNCINFVAMKFIIDNTLYFAEDDENLESD 36
 DB 272 DNLGVPFSPKGDNSITVLLBPDQYGN 300

RESULT 25
 US-09-764-864-1231
 Sequence 1231, Application US/09764864
 Patent No. US20020132753A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PT223
 CURRENT APPLICATION NUMBER: US/09/764,864
 CURRENT FILING DATE: 2001-01-17
 PRIOR APPLICATION data removed - consult PAM or file wrapper
 NUMBER OF SEQ ID NOS: 1792
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1231
 LENGTH: 151
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (148)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-764-864-1231

Query Match 27.7%; Score 52; DB 9; Length 151;
 Best Local Similarity 31.8%; Pred. No. 23;
 Matches 7; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAEPVEDNCFVAMKFIIDNT 22
 DB 122 LSVNIBESCFQFLKFKFDST 143

RESULT 26
 US-09-864-761-33630
 Sequence 33630, Application US/09864761
 Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Aeonica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03

DB 6 EDSCNFKEMFIDNTLYFIPEBNGDLESD 35

RESULT 18

US-10-895-396-12

Sequence 12, Application US/10895396
Publication No. US20050063945A1
GENERAL INFORMATION:
APPLICANT: Paul, Stephane
TITLE OF INVENTION: Novel Multifunctional Cytokines
FILE REFERENCE: 033751-096
CURRENT APPLICATION NUMBER: US/10/895,396
CURRENT FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: US 60/539,320
PRIOR FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: EPO 03 36 0086.7
PRIOR FILING DATE: 2003-07-21
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 371
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: fusion murine IL-2/linker/murine pro IL-18

US-10-895-396-12

Query Match 58.5%; Score 110; DB 17; Length 371;
Best Local Similarity 66.7%; Pred. No. 4,4e-07;
Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

DB 7 EDNCINFVAMKFIDNTLYFIADDDNLESD 36

185 EDSCNFKEMFIDNTLYFIPEBNGDLESD 214

RESULT 19

US-10-895-396-13

Sequence 13, Application US/10895396
Publication No. US20050063945A1
GENERAL INFORMATION:
APPLICANT: Paul, Stephane
TITLE OF INVENTION: Novel Multifunctional Cytokines
FILE REFERENCE: 032751-096
CURRENT APPLICATION NUMBER: US/10/895,396
CURRENT FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: US 60/539,320
PRIOR FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: EPO 03 36 0086.7
PRIOR FILING DATE: 2003-07-21
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 371
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: fusion murine IL-2/linker/murine pro IL-18 K69A

US-10-895-396-13

Query Match 58.5%; Score 110; DB 17; Length 371;
Best Local Similarity 66.7%; Pred. No. 4,4e-07;
Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

DB 7 EDNCINFVAMKFIDNTLYFIADDDNLESD 36

185 EDSCNFKEMFIDNTLYFIPEBNGDLESD 214

RESULT 20
US-10-369-493-3839

Sequence 3839, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3839
LENGTH: 1116
TYPE: PRT
ORGANISM: Neurospora crassa
FEATURES:
NAME/KEY: unsure
LOCATION: (1) (1116)
OTHER INFORMATION: unsure at all Xaa locations

US-10-369-493-3839

Query Match 29.8%; Score 56; DB 15; Length 1116;
Best Local Similarity 41.4%; Pred. No. 64;
Matches 12; Conservative 6; Mismatches 7; Indels 4; Gaps 1;

DB 5 PVEDNCINFVAMKFIDNTLYFIADDDNLESD 33

455 PDEENMVN---KVFENALASLEDDNLT 479

RESULT 21

US-10-424-599-240517

Sequence 240517, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 240517
LENGTH: 108
TYPE: PRT
ORGANISM: Glycine max
FEATURES:
OTHER INFORMATION: Clone ID: PAT_MRT3847_59214C.1.pcp

US-10-424-599-240517

Query Match 29.5%; Score 55.5; DB 15; Length 108;
Best Local Similarity 32.6%; Pred. No. 5;
Matches 14; Conservative 6; Mismatches 4; Indels 19; Gaps 2;

DB 6 VEDNCINFVAMKFIDNTLYFIADDDNLESD 29

52 VDNDCINFVAMKFIDNTLYFIADDDNLESD 94

RESULT 22

US-10-369-493-1397

Sequence 1397, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.

PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 133
TYPE: PRT
ORGANISM: Felis catus
FEATURE:
NAME/KEY: misc feature
LOCATION: (119)..(119)
OTHER INFORMATION: The 'Xaa' at location 119 stands for Lys, or Asn.
NAME/KEY: misc feature
LOCATION: (470)..(470)
OTHER INFORMATION: n = unknown at position 470
OTHER INFORMATION: Xaa = unknown at position 119
US-09-917-265-2

Query Match 74.2%; Score 139.5; DB 9; Length 133;
Best Local Similarity 75.0%; Pred. No. 9.2e-12;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MAAPVEDNCINPVAMKFIINTLYPIAEDDENTLSD 36
DB 1 MTAIPVDD-CINPVGMKFIINTLYPIVADSDENLETD 35

RESULT 15
US-09-917-265-8
Sequence 8, Application US/09917265
Patent No. US20020052030A1
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Borowski, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
FILE REFERENCE: IN-5
CURRENT APPLICATION NUMBER: US/09/917,265
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 192
TYPE: PRT
ORGANISM: Felis catus
US-09-917-265-8

Query Match 74.2%; Score 139.5; DB 9; Length 192;
Best Local Similarity 75.0%; Pred. No. 1.4e-11;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MAAPVEDNCINPVAMKFIINTLYPIAEDDENTLSD 36
DB 1 MTAIPVDD-CINPVGMKFIINTLYPIVADSDENLETD 35

RESULT 16
US-09-770-528-9
Sequence 9, Application US/09770528
Patent No. US20020164332A1
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
Sana, Theodore R.
Bazan, Fernando J.
Kaschelein, Robert A.
TITLE OF INVENTION: Mammalian Cytokines, Related Reagents
and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California
CITY: Palo Alto

STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,528
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/130,972
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/055,111
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: US 09/062,866
FILING DATE: 20-APR-1998
APPLICATION NUMBER: US 09/097,976
FILING DATE: 16-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0725K2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-770-528-9

Query Match 58.5%; Score 110; DB 9; Length 192;
Best Local Similarity 66.7%; Pred. No. 2e-07;
Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 EDNCINPVAMKFIINTLYPIAEDDENTLSD 36
DB 6 EDCVNFVKEMMFIDNTLYPIPEENGDLSD 35

RESULT 17
US-10-105-080-5
Sequence 5, Application US/10105080
Publication No. US20030143203A1
GENERAL INFORMATION:
APPLICANT: SAMTANG GENEX CORPORATION
TITLE OF INVENTION: RECOMBINANT ADENOVIRUSES EXPRESSING INTERLEUKIN-18 PROTEIN AND
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/105,080
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: KR 10-2001-78296
PRIOR FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Kopatentin 1.71
SEQ ID NO 5
LENGTH: 192
TYPE: PRT
ORGANISM: mouse interleukin-18 precursor mutant
US-10-105-080-5

Query Match 58.5%; Score 110; DB 14; Length 192;
Best Local Similarity 66.7%; Pred. No. 2e-07;
Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 EDNCINPVAMKFIINTLYPIAEDDENTLSD 36

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLESD 36
 DB 169 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLESD 204

RESULT 10
 US-10-094-153-3
 ; Sequence 3, Application US/10094153
 ; Publication No. US20020169291A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dinarello, Charles
 ; APPLICANT: Kim, Soo Hyun
 ; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use
 ; FILE REFERENCE: 475
 ; CURRENT APPLICATION NUMBER: US/10/094,153
 ; CURRENT FILING DATE: 2002-03-08
 ; PRIOR APPLICATION NUMBER: 60/274,327
 ; PRIOR FILING DATE: 2001-03-08
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic PRT Sequence
 US-10-094-153-3

Query Match 93.6%; Score 176; DB 13; Length 193;
 Best Local Similarity 97.1%; Pred. No. 1e-16;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34
 DB 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34

RESULT 11
 US-10-094-153-4
 ; Sequence 4, Application US/10094153
 ; Publication No. US20020169291A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dinarello, Charles
 ; APPLICANT: Kim, Soo Hyun
 ; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use
 ; FILE REFERENCE: 475
 ; CURRENT APPLICATION NUMBER: US/10/094,153
 ; CURRENT FILING DATE: 2002-03-08
 ; PRIOR APPLICATION NUMBER: 60/274,327
 ; PRIOR FILING DATE: 2001-03-08
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic PRT Sequence
 US-10-094-153-4

Query Match 93.6%; Score 176; DB 13; Length 193;
 Best Local Similarity 97.1%; Pred. No. 1e-16;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34
 DB 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34

RESULT 12
 US-10-094-153-5

; Sequence 5, Application US/10094153
 ; Publication No. US20020169291A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dinarello, Charles
 ; APPLICANT: Kim, Soo Hyun
 ; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use
 ; FILE REFERENCE: 475
 ; CURRENT APPLICATION NUMBER: US/10/094,153
 ; CURRENT FILING DATE: 2002-03-08
 ; PRIOR APPLICATION NUMBER: 60/274,327
 ; PRIOR FILING DATE: 2001-03-08
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic PRT Sequence
 US-10-094-153-5

Query Match 93.6%; Score 176; DB 13; Length 193;
 Best Local Similarity 97.1%; Pred. No. 1e-16;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34
 DB 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34

RESULT 13
 US-10-094-153-9
 ; Sequence 9, Application US/10094153
 ; Publication No. US20020169291A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dinarello, Charles
 ; APPLICANT: Kim, Soo Hyun
 ; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use
 ; FILE REFERENCE: 475
 ; CURRENT APPLICATION NUMBER: US/10/094,153
 ; CURRENT FILING DATE: 2002-03-08
 ; PRIOR APPLICATION NUMBER: 60/274,327
 ; PRIOR FILING DATE: 2001-03-08
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic PRT Sequence
 US-10-094-153-9

Query Match 93.6%; Score 176; DB 13; Length 193;
 Best Local Similarity 97.1%; Pred. No. 1e-16;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34
 DB 1 MAABPEVDNCINPVAMKFIIDNTLYFIAEDDENLE 34

RESULT 14
 US-09-917-265-2
 ; Sequence 2, Application US/09917265
 ; Patent No. US20020052030A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wonderling, Ramani S.
 ; APPLICANT: Boroschs, Karen L.
 ; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
 ; FILE REFERENCE: 1W-5
 ; CURRENT APPLICATION NUMBER: US/09/917,265
 ; CURRENT FILING DATE: 2001-07-27

SEQ ID NO 5
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-10-679-201-5

Query Match 100.0%; Score 188; DB 16; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFAVAMKFIIDNTLYFAEDDENLESD 36
DB 1 MAAPVEDNCINFAVAMKFIIDNTLYFAEDDENLESD 36

RESULT 6
US-10-646-308-13
Sequence 13, Application US/10646308
Publication No. US20040136992A1
GENERAL INFORMATION:
APPLICANT: BURTON, Paul B. J.
APPLICANT: DEISHER, Theresa A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE
FILE REFERENCE: 3432-B
CURRENT APPLICATION NUMBER: US/10/646,308
PRIOR FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: --to be assigned--
PRIOR FILING DATE: 2003-08-12
PRIOR APPLICATION NUMBER: 60/406,418
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.2
SEQ ID NO 13
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (73)..(73)
OTHER INFORMATION: The 'Xaa' at location 73 stands for Thr, or Ile.
US-10-646-308-13

Query Match 100.0%; Score 188; DB 16; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFAVAMKFIIDNTLYFAEDDENLESD 36
DB 1 MAAPVEDNCINFAVAMKFIIDNTLYFAEDDENLESD 36

RESULT 7
US-10-823-964A-3
Sequence 3, Application US/10823964A
Publication No. US2005008615A1
GENERAL INFORMATION:
APPLICANT: BAM, NARENDRA
APPLICANT: BONGERS, JACOB
APPLICANT: KIRKPATRICK, ROBERT B.
APPLICANT: JANSON, CHERYL A.
APPLICANT: JOHANSON, KTRUNG
APPLICANT: QIU, XIANYANG
TITLE OF INVENTION: CONJUGATES COMPRISING HUMAN IL-18 AND
FILE REFERENCE: PU60053
CURRENT APPLICATION NUMBER: US/10/823,964A
PRIOR FILING DATE: 2004-04-14
PRIOR APPLICATION NUMBER: 60/162,947
PRIOR FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3

LENGTH: 203
TYPE: PRT
ORGANISM: Homo sapiens
US-10-823-964A-3

Query Match 100.0%; Score 188; DB 17; Length 203;
Best Local Similarity 100.0%; Pred. No. 2.2e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFAVAMKFIIDNTLYFAEDDENLESD 36
DB 1 MAAPVEDNCINFAVAMKFIIDNTLYFAEDDENLESD 46

RESULT 8
US-10-895-396-8
Sequence 8, Application US/10895396
Publication No. US20050063945A1
GENERAL INFORMATION:
APPLICANT: Paul, Stephanie
TITLE OF INVENTION: Novel Multifunctional Cytokines
FILE REFERENCE: 032751-096
CURRENT APPLICATION NUMBER: US/10/895,396
CURRENT FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: US 60/539,320
PRIOR FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: EPO 03 36 0086.7
PRIOR FILING DATE: 2003-07-21
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 361
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion human IL-2/linker/human pro IL-18
US-10-895-396-8

Query Match 100.0%; Score 188; DB 17; Length 361;
Best Local Similarity 100.0%; Pred. No. 4.3e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFAVAMKFIIDNTLYFAEDDENLESD 36
DB 169 MAAPVEDNCINFAVAMKFIIDNTLYFAEDDENLESD 204

RESULT 9
US-10-895-396-9
Sequence 9, Application US/10895396
Publication No. US20050063945A1
GENERAL INFORMATION:
APPLICANT: Paul, Stephanie
TITLE OF INVENTION: Novel Multifunctional Cytokines
FILE REFERENCE: 032751-096
CURRENT APPLICATION NUMBER: US/10/895,396
CURRENT FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: US 60/539,320
PRIOR FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: EPO 03 36 0086.7
PRIOR FILING DATE: 2003-07-21
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 361
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion human IL-2/linker/human pro IL-18 K89A
US-10-895-396-9

Query Match 100.0%; Score 188; DB 17; Length 361;
Best Local Similarity 100.0%; Pred. No. 4.3e-18;

GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
Sana, Theodore R.
Bazan, Fernando J.
Kastelnick, Robert A.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSER: DNAX Research Institute
STREET: 901 California
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,528
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/130,972
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/055,111
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: US 09/062,866
FILING DATE: 20-APR-1998
APPLICATION NUMBER: US 09/097,976
FILING DATE: 16-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0725K2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULAR TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-770-528-8

Query Match 100.0%; Score 188; DB 9; Length 193;
Best Local Similarity 100.0%; Pred. No. 2,1e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIIDNTLYFLAEDDENLESD 36
DB 1 MAAPVEDNCINFVAMKFIIDNTLYFLAEDDENLESD 36

RESULT 3
US-10-311-491-1
Sequence 1, Application US/10311491
Publication No. US20030143198A1
GENERAL INFORMATION:
APPLICANT: Johnson, Kyung O.
APPLICANT: Kirkpatrick, Robert B.
APPLICANT: Shetman, Allan R.
APPLICANT: Ho, Yen Sen
APPLICANT: McDevitt, Damien
TITLE OF INVENTION: Method for Preparing a Physiologically
Active IL-18 Polypeptide
FILE REFERENCE: P51137
CURRENT APPLICATION NUMBER: US/10/311,491

CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/US01/18804
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/211,832
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/224,128
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/264,923
PRIOR FILING DATE: 2001-01-20
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapien
US-10-311-491-1

Query Match 100.0%; Score 188; DB 14; Length 193;
Best Local Similarity 100.0%; Pred. No. 2,1e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIIDNTLYFLAEDDENLESD 36
DB 1 MAAPVEDNCINFVAMKFIIDNTLYFLAEDDENLESD 36

RESULT 4
US-10-105-080-4
Sequence 4, Application US/10105080
Publication No. US20030143203A1
GENERAL INFORMATION:
APPLICANT: SAMYANG GENEX CORPORATION
TITLE OF INVENTION: RECOMBINANT ADENOVIRUSES EXPRESSING INTERLEUKIN-18 PROTEIN AND
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/105,080
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: KR 10-2001-78296
PRIOR FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4
LENGTH: 193
TYPE: PRT
ORGANISM: Human Interleukin-18 precursor mutant
US-10-105-080-4

Query Match 100.0%; Score 188; DB 14; Length 193;
Best Local Similarity 100.0%; Pred. No. 2,1e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPVEDNCINFVAMKFIIDNTLYFLAEDDENLESD 36
DB 1 MAAPVEDNCINFVAMKFIIDNTLYFLAEDDENLESD 36

RESULT 5
US-10-679-201-5
Sequence 5, Application US/10679201
Publication No. US20040120923A1
GENERAL INFORMATION:
APPLICANT: DINARELLO, CHARLES A.
APPLICANT: KIM, SOO-HYUN
APPLICANT: BUFLER, PHILIP
TITLE OF INVENTION: METHOD OF TREATMENT USING A CYTOKINE ABLE TO BIND
FILE REFERENCE: 057878-000011
CURRENT APPLICATION NUMBER: US/10/679,201
CURRENT FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/446,827
PRIOR FILING DATE: 2002-10-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 3.2

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OM protein - protein search, using sw model

Run on: May 13, 2005, 12:25:20 / Search time 134 Seconds
(without alignments)
89.745 Million cell updates/sec.

Title: US-09-711-896a-1

Perfect score: 188
Sequence: 1 MAABPVEDNCINFPVAKKFIIDNTLYFAEDDENLESD 36

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1432185 seqs, 334051727 residues 1432185

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/2/pubppa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	188	100.0	193	9	US-09-798-075-1
2	188	100.0	193	9	US-09-770-528-8
3	188	100.0	193	14	US-10-111-491-1
4	188	100.0	193	14	US-10-105-080-4
5	188	100.0	193	16	US-10-679-201-5
6	188	100.0	193	16	US-10-646-308-13
7	188	100.0	203	17	US-10-823-964A-3
8	188	100.0	361	17	US-10-895-396-9
9	188	100.0	361	17	US-10-895-396-9
10	176	93.6	193	13	US-10-094-153-3
11	176	93.6	193	13	US-10-094-153-4
12	176	93.6	193	13	US-10-094-153-5
13	176	93.6	193	13	US-10-094-153-9

14	139.5	74.2	133	9	US-09-917-265-2	Sequence 2, Appl1
15	139.5	74.2	192	9	US-09-917-265-8	Sequence 8, Appl1
16	110	58.5	192	9	US-09-770-528-9	Sequence 9, Appl1
17	110	58.5	192	14	US-10-105-080-5	Sequence 5, Appl1
18	110	58.5	371	17	US-10-895-396-12	Sequence 12, Appl1
19	110	58.5	371	17	US-10-895-396-13	Sequence 13, Appl1
20	56	29.8	1116	15	US-10-369-493-3839	Sequence 3839, Ap
21	55.5	29.5	108	15	US-10-424-599-240517	Sequence 240517,
22	55	29.3	687	15	US-10-369-493-1397	Sequence 1397, Ap
23	54	28.7	81	16	US-10-872-874-158	Sequence 158, App
24	53	28.2	679	15	US-10-369-493-11186	Sequence 11186, A
25	52	27.7	151	9	US-09-764-864-1231	Sequence 1231, Ap
26	52	27.7	156	9	US-09-864-761-33630	Sequence 33630, A
27	52	27.7	445	9	US-09-864-761-46601	Sequence 46601, A
28	52	27.7	736	9	US-09-864-761-47605	Sequence 47605, A
29	52	27.7	745	15	US-10-170-385-285	Sequence 285, App
30	51.5	27.4	383	15	US-10-369-493-20614	Sequence 20614, A
31	50.5	26.9	224	16	US-10-437-963-150952	Sequence 150952,
32	50.5	26.9	1083	16	US-10-437-963-150950	Sequence 150950,
33	50	26.6	78	9	US-09-749-637A-318	Sequence 318, App
34	50	26.6	438	15	US-10-424-599-174564	Sequence 174564,
35	50	26.6	536	14	US-10-087-167-14	Sequence 14, Appl1
36	50	26.6	536	15	US-10-606-060A-9	Sequence 9, Appl1
37	50	26.6	663	16	US-10-437-963-111822	Sequence 111822,
38	49.5	26.3	185	16	US-10-363-823-363	Sequence 363, App
39	49.5	26.3	380	15	US-10-369-493-13822	Sequence 13822, A
40	49.5	26.3	547	15	US-10-363-616-488	Sequence 488, App
41	49.5	26.3	568	15	US-10-282-122A-57666	Sequence 57666, A
42	49.5	26.3	568	16	US-10-437-963-134407	Sequence 134407,
43	49	26.1	285	9	US-09-815-242-4869	Sequence 4869, Ap
44	49	26.1	295	15	US-10-282-122A-42529	Sequence 42529, A
45	49	26.1	334	9	US-09-815-242-10798	Sequence 10798, A

ALIGNMENTS

RESULT 1
US-09-798-075-1
Sequence 1, Application US/09798075
Patent No. US2001004418A1
GENERAL INFORMATION:
APPLICANT: Levy, Shoshana
APPLICANT: Dekruiff, Rosemarie
APPLICANT: Umetau, Dale
APPLICANT: Maecker, Holden
TITLE OF INVENTION: Treatment of Allergies
FILE REFERENCE: STAN-179
CURRENT APPLICATION NUMBER: US/09/798, 075
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/188, 311
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-09-798-075-1

Query Match 100.0% Score 188, DB 9, Length 193;
Best Local Similarity 100.0%; Pred. No. 2, 1e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAABPVEDNCINFPVAKKFIIDNTLYFAEDDENLESD 36
DB 1 MAABPVEDNCINFPVAKKFIIDNTLYFAEDDENLESD 36

RESULT 2
US-09-770-528-8
Sequence 8, Application US/09770528
Patent No. US20020164332A1

A/Map position: 1p21-1p21
 A/Intons: 561/3, 579/3, 597/3, 615/3, 633/3, 648/3, 666/3, 681/3
 A/Note: the 11st of intons is incomplete
 C/Complex: type XI collagen may be a heterotrimer of two alpha 1(XI) chains and one alpha 3(XI) chain (see PIR:CGH06C), initially linked by disulfide bonds among their carboxyl-termini with desmosine cross-links made from lysine and allysine residues
 C/Function:
 A/Description: structural component of extracellular fibrous polymer associated with cell A/Note: may play a role in controlling the lateral growth of collagen II fibrils
 C/Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology
 C/Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyproline
 F/1-36/Domain: signal sequence #status predicted <SIG>
 F/35-266/Domain: PARP-like #status predicted <PARP>
 F/37-511/Domain: amino-terminal propeptide #status predicted <PRO>
 F/512-1565/Produce: collagen alpha 1(XI) chain #status predicted <MAT>
 F/512-557/Region: amino-terminal nonhelical telopeptide
 F/528-1542/Region: helical
 F/1543-1565/Region: carboxyl-terminal nonhelical telopeptide
 F/1566-1806/Domain: fibrillar collagen carboxyl-terminal homology <CTP>
 F/1583-1806/Domain: fibrillar collagen carboxyl-terminal homology <CTP>
 F/61-243,112-236/Disulfide bonds: #status predicted
 F/505/Modified site: allysine (Lys) #status predicted
 F/612,1452/Modified site: 5-hydroxylysine (Lys) #status predicted
 F/612,1452/Binding site: carbohydrate (Lys) (covalent) #status predicted

Query Match 25.0%; Score 47.5; DB 1; Length 1806;
 Best Local Similarity 23.3%; Pred. No. 4.2e+02;
 Matches 14; Conservative 4; Mismatches 13; Indels 29; Gaps 1;

QY 6 VEDNCINFVAMKPF-----DNTLYFIADDDNLESD 36
 DB 1686 VEGNSIMVQNTFKLITASARQNTYHCQSAAMVDVSSGYDKALFLGSDNDEMSYD 1745

RESULT 39
 S69031
 hypothetical protein YPR143w - yeast (Saccharomyces cerevisiae)
 C/Species: Saccharomyces cerevisiae
 C/Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C/Accession: S69031
 R/Pulten, L.
 submitted to the EMBL Data Library, November 1995
 A/Description: The sequence of S. cerevisiae cosmid 9659.
 A/Reference number: S69022
 A/Accession: S69031
 A/Molecule type: DNA
 A/Residues: 1-250 <FTL>
 A/Cross-references: UNIPROT:Q06511; EMBL:U40829; NID:g1066476; PID:g1066480; GSPDB:GN000
 C/Genetics:
 A/Genes: MIPS:YPR143w
 A/Cross-references: SGD:S0006347
 A/Map position: 16R

Query Match 25.0%; Score 47; DB 2; Length 250;
 Best Local Similarity 38.2%; Pred. No. 61;
 Matches 13; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 3 ABEVDNCINFVAMKPFIDNTLYFIADDDNLESD 36
 DB 48 ABEDEQNSSDSBSKIDNQSDAEDDDEED 81

RESULT 40
 S75062
 transcription regulator of rubisco operon - Synechocystis sp. (strain PCC 6803)
 N/Alternate names: protein sll1594
 C/Species: Synechocystis sp.
 A/Variety: PCC 6803
 C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C/Accession: S75062
 R/Kaneke, T.; Sato, S.; Kocant, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 B.
 A/Reference number: S74322; MUID:97061201; PMID:8905231
 A/Accession: S75062
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-316 <KAN>
 A/Cross-references: UNIPROT:P73862; EMBL:D90910; GB:AB001339; NID:g1652956; PID:BA1792
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C/Genetics:
 A/Genes: rbcR
 C/Superfamily: transcription activator LysR-type

Query Match 25.0%; Score 47; DB 2; Length 316;
 Best Local Similarity 36.4%; Pred. No. 78;
 Matches 12; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

QY 1 MAEPVDNCINFVAMKPFIDNTLYFIADDDNLESD 33
 DB 146 IVSEPEIDILNY--QPLDNPVIVARRDHP 176

Search completed: May 13, 2005, 12:25:56
 Job time: 40 secs

submitted to the EMBL Data Library, November 1995

A>Description: The sequence of C. elegans comid C18B2.

A.Reference number: Z18368

A.Accession: J15551

A.Status: preliminary/ translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-673 <STE>

A.Cross-references: UNIPROT:Q18076; EMBL:U0413; NID:g1065467; PID:g1065470; PIDN:AAA814

C/Genetics:

A.Gene: CESP:C18B2.5

A.Introns: 31/3; 101/3; 182/3; 214/1; 269/3; 372/1; 399/3; 474/2; 528/3; 640/3

C.Superfamily: Caenorhabditis elegans hypothetical protein C18B2.5

Query Match 25.3%; Score 47.5; DB 2; Length 673;

Best Local Similarity 27.5%; Pred. No. 1.5e+02;

Matches 14; Conservative 8; Mismatches 10; Indels 19; Gaps 2;

Qy 3 AEVDNDCINPV-----AMKFDNTYFIADENLESD 36

Db 91 ATPVDDIMNSVSAVTPTVNLHGHDALHLEALY--GEDEHSIVSE 139

RESULT 35

collagen alpha 1(XI) chain - chicken (fragment)

C/Species: Gallus gallus (chicken)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S28791

R/NaH. H.D. Barenbaum, M.; Upholt, W.B.

J. Biol. Chem. 267, 22581-22586, 1992

A>Title: The chicken alpha1(XI) collagen gene is widely expressed in embryonic tissues.

A.Reference number: S28791; MUID:93054557; PMID:1429607

A.Accession: S28791

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-888 <NA>

A.Cross-references: UNIPROT:Q90796; EMBL:M88593; NID:g211619; PIDN:AAA48707.1; PID:g2116

C.Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology

F/665-887/Domain: fibrillar collagen carboxyl-terminal homology <FCC>

Query Match 25.3%; Score 47.5; DB 2; Length 888;

Best Local Similarity 23.3%; Pred. No. 2e+02;

Matches 14; Conservative 4; Mismatches 13; Indels 29; Gaps 1;

Qy 6 VEDNCINPVAMKFI-----DNTLYFIADENLESD 36

Db 768 VEGNINNVQTFRLKLSASRQNTYCHQSVAMHDASSDYDAKLFSGNDHEMDYD 827

RESULT 36

DNA polymerase III - Mycoplasma pulmonis

C/Species: Mycoplasma pulmonis

C/Date: 06-Sep-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S54697; S49397

R/Barnes, M.H.; Tarranto Jr., P.M.; Spaccapoli, P.; Brown, N.C.; Yu, H.; Dybvig, K.

Mol. Microbiol. 13, 843-854, 1994

A>Title: DNA polymerase III of Mycoplasma pulmonis: isolation and characterization of th

A.Reference number: S54697; MUID:93115554; PMID:781943

A.Accession: S54697

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-1435 <BAR>

A.Cross-references: UNIPROT:P47729; EMBL:U06833; NID:g487435; PIDN:AAA18178.1; PID:g4874

R/Dybvig, K.; Yu, H.

Mol. Microbiol. 12, 547-560, 1994

A>Title: Regulation of a restriction and modification system via DNA inversion in Mycopl

A.Reference number: S49397; MUID:95020589; PMID:7934878

A.Accession: S49397

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1408-1435 <DYB>

A.Cross-references: GB:L25415; NID:g496153; PIDN:AAA65635.1; PID:g496160

C/Genetics:

A.Gene: code: SGC3

C.Superfamily: DNA-directed DNA polymerase III alpha chain polC

Query Match 25.3%; Score 47.5; DB 2; Length 1435;

Best Local Similarity 48.0%; Pred. No. 3.3e+02;

Matches 12; Conservative 3; Mismatches 7; Indels 3; Gaps 1;

Qy 12 NFVAMKFDNTLYF--IAEDENL 33

Db 495 NFKQKFDNNIBFEMISIDTLNL 519

RESULT 37

hypothetical protein MYPV 6750 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C/Species: Mycoplasma pulmonis

C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C/Accession: C90596

R/Chambaud, I.; Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A>Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulr

A.Reference number: A99512; MUID:21267165; PMID:11353084

A.Accession: C90596

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-1435 <KUR>

A.Cross-references: UNIPROT:P47729; GB:A445566; PID:g14090090; PIDN:CAC13848.1; GSPDB:C

A.Experimental source: strain UAB CTIP

C/Genetics:

A.Gene: MYPV 6750

A.Gene: code: SGC3

C.Superfamily: DNA-directed DNA polymerase III alpha chain polC

Query Match 25.3%; Score 47.5; DB 2; Length 1435;

Best Local Similarity 48.0%; Pred. No. 3.3e+02;

Matches 12; Conservative 3; Mismatches 7; Indels 3; Gaps 1;

Qy 12 NFVAMKFDNTLYF--IAEDENL 33

Db 495 NFKQKFDNNIBFEMISIDTLNL 519

RESULT 38

CGHUL

collagen alpha 1(XI) chain precursor - human

N/Alternate names: procollagen alpha 1(XI) chain

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1990 #sequence_revision 03-Oct-1995 #text_change 08-May-1998

C/Accession: A35239; A31795

R/Yoshioaka, H.; Ramirez, F.

J. Biol. Chem. 265, 6423-6426, 1990

A>Title: Pro-alpha1(XI) collagen. Structure of the amino-terminal propeptide and express

A.Reference number: A35239; MUID:9020924; PMID:1690726

A.Accession: A35239

A.Molecule type: mRNA

A.Residues: 1-558 <YOS>

A.Cross-references: GB:J05407

R/Bernard, M.; Yoshioaka, H.; Rodriguez, E.; van der Rest, M.; Kimura, T.; Ninomiya, Y.;

J. Biol. Chem. 263, 17159-17166, 1988

A>Title: Cloning and sequencing of pro-alpha1(XI) collagen cDNA demonstrates that type X

cartilaginous tissue.

A.Reference number: A92689; MUID:89034222; PMID:3182841

A.Accession: A31795

A.Molecule type: DNA; mRNA

A.Residues: 538-1806 <BER>

A.Cross-references: GB:J04177

A>Note: parts of this sequence were determined by protein sequencing

C/Comment: Prolines and lysines at the third position of the tripeptide repeating unit (

ed and subsequently O-glycosylated.

C/Genetics:

A.Gene: GDB:COL1A1; COL16

A.Cross-references: GDB:120595; OMIM:120280


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RESULT 26
S71376
glutamate receptor homolog - cherry salmon
C/Species: Oncorhynchus masou (cherry salmon)
C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C/Accession: S71376
R/Kubokawa, K., Miyashita, T., Nagasawa, H., Kubo, Y.
P/BSL Letc. 392, 71-76, 1996
A/Title: Cloning and characterization of a bifunctional metabotropic receptor activated
A/Reference number: S71376; PMID:8769318
A/Accession: S71376
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-1218 <KUB>
A/Cross-References: UNIPROT:Q902F3
C/Keywords: glycoprotein; phosphoprotein
P/603-623/Domain: transmembrane #status predicted <TM1>
P/640-660/Domain: transmembrane #status predicted <TM2>
P/672-690/Domain: transmembrane #status predicted <TM3>
P/717-737/Domain: transmembrane #status predicted <TM4>
P/761-782/Domain: transmembrane #status predicted <TM5>
P/796-817/Domain: transmembrane #status predicted <TM6>
P/826-850/Domain: transmembrane #status predicted <TM7>
P/104-233-403-525-757/Binding site: carbohydrate (Asn) (covalent) #status predicted
P/636-699-961/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status pre
P/705/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
P/892/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predic

Query Match          25.8%; Score 48.5; DB 2; Length 1218;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 11; Conservative 5; Mismatches 3; Indels 3; Gaps 1;

Qy 14 VAMKPID--NLTLYFAEDDEN 32
DB 953 VAMKPIDSTKTLVNAEDES 974

RESULT 27
S18253
laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C/Accession: S28399; S18253
R/Kusche-Gulberg, M., Garrison, K., Mackrell, A.J., Fessler, L.I., Fessler, J.H.
EMBO J. 11, 4519-4527, 1992
A/Title: Laminin A chain: expression during Drosophila development and genomic sequence.
A/Reference number: S28399; PMID:93049203; PMID:1425586
A/Accession: S28399
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-3712 <KUS>
A/Cross-References: UNIPROT:O00174; GB:M96388; NID:g157799; PIDN:AAA2662.1; PID:g157800
R/Garrison, K., Mackrell, A.J., Fessler, J.H.
U. Biol. Chem. 266, 22899-22904, 1991
A/Title: Drosophila laminin A chain sequence, interspecies comparison, and domain struct
A/Reference number: S18253; PMID:92078147; PMID:1744083
A/Accession: S18253
A/Molecule type: mRNA
A/Residues: 1762-3712 <GAR>
A/Cross-References: EMBL:M75882; NID:g157797; PIDN:AAA2661.1; PID:g157798
C/Genetics:
A/Gene: FLYBase:lanA
A/Cross-References: FlyBase:FBgn0002526
C/Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
F/273-330/Domain: laminin-type EGF-like homology <LEG>
C/Keyword: basement membrane; cell binding; coiled coil; disulfide bond; extracellular
F/333-400/Domain: laminin-type EGF-like homology <LEG2>
F/541-584/Domain: laminin-type EGF-like homology <LEG3>
F/1776-2115/Domain: III <DOM3>
F/1776-2115/Domain: laminin-type EGF-like homology <LEG4>
F/1809-1866/Domain: laminin-type EGF-like homology #status atypical <LE1>
F/1859-1914/Domain: laminin-type EGF-like homology <LE2>
F/1859-1914/Domain: laminin-type EGF-like homology <LE3>
F/1917-1967/Domain: laminin-type EGF-like homology <LE4>

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F/1970-2014/Domain: laminin-type EGF-like homology <LE5>
F/2017-2061/Domain: laminin-type EGF-like homology <LE6>
F/2064-2109/Domain: laminin-type EGF-like homology <LE7>
F/2116-2697/Domain: laminin-type EGF-like homology <LE7>
F/2698-2863/Domain: G <DOMG>
F/2698-2863/Domain: repeat G1 <RG1>
F/2864-3048/Domain: repeat G2 <RG2>
F/3049-3223/Domain: repeat G3 <RG3>
F/3079-3200/Domain: laminin G repeat homology <LG3>
F/3334-3528/Domain: repeat G4 <RG4>
F/3529-3712/Domain: repeat G5 <RG5>
F/1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,3

Query Match          25.8%; Score 48.5; DB 2; Length 3712;
Best Local Similarity 36.0%; Pred. No. 6.6e+02;
Matches 9; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

Qy 12 NFVAMKPIDNTLYFAEDD-ENLES 35
DB 3580 SYALIELVDNTLYFTVKTDLKNIVS 3604

RESULT 28
H90128
hypothetical protein orf209 (imported) - Guillardia theta nucleomorph
C/Species: nucleomorph Guillardia theta
A/Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H90128
R/Douglas, S., Zauner, S., Fraunholz, M., Beaton, M., Penny, S., Deng, L.T., Wu, X., Rei
Nature 410, 1091-1096, 2001
A/Title: The highly reduced genome of an enslaved algal nucleus.
A/Reference number: A99082; PMID:11323671; PMID:11323671
A/Accession: H90128
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-209 <DOU>
A/Cross-References: UNIPROT:Q98659; GB:AF083031; NID:g13794346; PIDN:AAK9723.1; GSPDB:G
C/Genetics:
A/Gene: orf209
A/Map position: 3
A/Genome: nucleomorph
C/Keywords: nucleomorph

Query Match          25.5%; Score 48; DB 2; Length 209;
Best Local Similarity 43.5%; Pred. No. 37;
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 12 NFVAMKPIDNTLYFAEDDENLE 34
DB 85 NFIIINSIIKFFFIEDDGNIE 107

RESULT 29
T34102
hypothetical protein C17G10.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T34102
R/Johnson, D.
submitted to the EMBL Data Library, June 1995
A/Description: The sequence of C. elegans cosmid C17G10.
A/Reference number: Z21476
A/Accession: T34102
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-480 <JOH>
A/Cross-References: UNIPROT:Q09973; EMBL:U28739; PIDN:AAK93451.1; GSPDB:GN00020; CESP:CI
A/Experimental source: strain Bristol N2; clone C17G10
C/Genetics:
A/Gene: CESP:C17G10.1
A/Map position: 2
A/Introns: 51/1, 116/2, 158/3, 191/1, 299/3, 430/3

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A/Map position: 1L

Query Match 26.1% Score 49; DB 2; Length 1628;
 Best Local Similarity 66.7%; Pred. No. 2.4e+02;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 21 NTLFYIADDDNLES 35
 DB 303 NLOIYKEDDENLES 317

RESULT 22

T09308

Immediate-early protein - human herpesvirus 6 (strain UI102)

C/Species: human herpesvirus 6

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C/Accession: T09308

R/Nicholas, J.; Martin, M.

J. Virol. 68, 597-610, 1994

A/Title: Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of hu

A/Reference number: Z16644; MUID:94118404; PMID:8289364

A/Accession: T09308

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-285 <NTC>

A/Cross-references: UNIPROT:Q89432; EMBL:L25528; NID:9451932; PIDN:AAA16721.1; PID:94519

C/Genetic8:

A/Genes: EHF2

C/Superfamily: human herpesvirus 6 transcription regulator B701

Query Match 25.8% Score 48.5; DB 2; Length 285;
 Best Local Similarity 28.2%; Pred. No. 44;
 Matches 11; Conservative 5; Mismatches 12; Indels 11; Gaps 1;

QY 4 EPVEDNCI-----NFVAKFIDNTLYFIADDE 31
 DB 49 EETRDVCLTKTIVFAGDEKFGDGFVNETIYLAETTE 87

RESULT 23

JC4374

sterol uptake protein 1 - Yeast (Saccharomyces cerevisiae)

N/Alternate names: protein G1828; Protein YGL162w; SUT1 protein

C/Species: Saccharomyces cerevisiae

C/Date: 10-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004

C/Accession: JC4374; S60424; S64178

R/Bourc, S.; Karet, F.

Gene 165, 97-102, 1995

A/Title: Isolation and characterization of the Saccharomyces cerevisiae SUT1 gene involv

A/Reference number: JC4374; MUID:96084960; PMID:7489925

A/Accession: JC4374

A/Molecule type: DNA

A/Residues: 1-299 <BOU>

A/Cross-references: UNIPROT:P53032; EMBL:X77766; NID:9183994; PIDN:CAAS4806.1; PID:9118

R/Tames, C.M.; Indge, K.J.; Oliver, S.G.

Yeast 11, 1413-1419, 1995

A/Title: DNA sequence analysis of a 35 kb segment from Saccharomyces cerevisiae chromosom

A/Reference number: S60417; MUID:9618061; PMID:8585324

A/Accession: S60424

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-299 <UAM>

A/Cross-references: EMBL:Z48618

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995

R/Tames, C.M.; Indge, K.J.; Oliver, S.G.

submitted to the Protein Sequence Database, May 1996

A/Reference number: S64165

A/Accession: S64178

A/Molecule type: DNA

A/Residues: 1-299 <JAM>

A/Cross-references: EMBL:Z72684; NID:91322757; PID:9243599; PID:91322758; MIPS:YGL162w

C/Comment: This protein is a member of the hypoxic gene family, and is rich in serine an

C/Genetics:

A/Genes: SGD:SUT1

A/Cross-references: SGD:S0003130; MIPS:YGL162w

A/Map position: 7L

C/Superfamily: Saccharomyces cerevisiae hypothetical protein YPR009w

F/13-151/Region: serine/threonine-rich

Query Match 25.8% Score 48.5; DB 2; Length 299;
 Best Local Similarity 33.3%; Pred. No. 46;
 Matches 13; Conservative 4; Mismatches 9; Indels 13; Gaps 2;

QY 5 PVBDNC-----INF--VAKFIDNTLYFIADDD 30
 DB 255 PKNDKCTFSKGFTRADINISSKSLKFKDITDITVD 293

RESULT 24

F81354

DNA/pantothenate metabolism flavoprotein Cj0822 (imported) - Campylobacter jejuni (stra

C/Species: Campylobacter jejuni

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C/Accession: F81354

R/Parthill, J.; Wren, B.W.; Mungall, K.; Kerley, J.M.; Churcher, C.; Basham, D.; Chillin

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barr

Nature 403, 665-668, 2000

A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A/Reference number: A81250; MUID:20150912; PMID:10688204

A/Accession: F81354

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-384 <PAR>

A/Cross-references: UNIPROT:Q9PPA1; GB:AL139076; GB:AL111168; NID:96968128; PIDN:CAB7308

A/Experimental source: serotype O2, strain NCTC 11168

C/Genetics:

A/Genes: dfr; Cj0822

C/Superfamily: pantothenate metabolism flavoprotein dfr

Query Match 25.8% Score 48.5; DB 2; Length 384;
 Best Local Similarity 30.0%; Pred. No. 60;
 Matches 12; Conservative 8; Mismatches 11; Indels 9; Gaps 1;

QY 2 AAEVBDNCINFAVAKFID-----NTLYFIADDDN 32
 DB 324 AKSLXDKOLDMVCLNIDQKVFSGDQNELVYITLNNEN 363

RESULT 25

WZVZG1

GIL protein - Amasacta moorei poxvirus

C/Species: Amasacta moorei poxvirus

C/Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

C/Accession: A41561

R/Hall, R.L.; Moyer, R.W.

J. Virol. 65, 6516-6527, 1991

A/Title: Identification, cloning, and sequencing of a fragment of Amasacta moorei entomop

A/Reference number: A41561; MUID:92046310; PMID:1942245

A/Accession: A41561

A/Molecule type: DNA

A/Residues: 1-464 <HAL>

A/Cross-references: UNIPROT:P29817; GB:W71782; NID:9209631; PIDN:AAA42379.1; PID:9209632

C/Superfamily: vaccinia virus 17 protein

C/Keywords: late protein

Query Match 25.8% Score 48.5; DB 1; Length 464;
 Best Local Similarity 57.9%; Pred. No. 73;
 Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVAKF---IDNTLYFI 26
 DB 20 INFMSLFLFSKIDNMVYFI 38

Db 147 AKTANDSINFSAADITLTL 170

RESULT 17

outer layer protein VP3 - simian rotavirus SA11 (fragment)

C/Species: simian rotavirus SA11

C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004

C/Accession: A04129

R/Lopez, S.; Arias, C.F.; Bell, J.R.; Straus, J.H.; Espajo, R.T.

Virology 144, 11-19, 1985

A/Title: Primary structure of the cleavage site associated with trypsin enhancement of

A/Reference number: A04129; MUID:86045932; PMID:2998038

A/Accession: A04129

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: genomic RNA

A/Residues: 1-747 <TOP>

A/Cross-references: UNIPROT:P04508; GB:M1158; NID:961868

C/Genetics:

A/Map position: segment 4

C/Superfamily: rotavirus outer layer protein VP3

Query Match 26.1%; Score 49; DB 1; Length 747;

Best Local Similarity 52.6%; Pred. No. 1e+02;

Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

17 KPIDNTLYPIADDENTLES 35

663 KPIPNRAYVIXDDEVLEA 681

RESULT 18

outer layer protein VP3 - bovine rotavirus A (strain C486)

C/Species: bovine rotavirus A

C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999

C/Accession: A23529

R/Porter, A.A.; Cox, G.; Parker, M.; Babiuk, L.A.

Nucleic Acids Res 15, 4361, 1987

A/Title: The complete nucleotide sequence of bovine rotavirus C486 gene 4 cDNA.

A/Reference number: A23529; MUID:8721020; PMID:3035492

A/Accession: A23529

A/Molecule type: genomic RNA

A/Residues: 1-776 <TOP>

A/Cross-references: GB:Y00127; NID:961854; PIDN:CAA68325.1; PID:961855

C/Genetics:

A/Map position: segment 4

C/Superfamily: rotavirus outer layer protein VP3

C/Keywords: glycoprotein, hemagglutinin

P/32,56,97,132,151,183,198,456,507,596,602/Binding site: carbohydrate (Asn) (covalent) #

Query Match 26.1%; Score 49; DB 1; Length 776;

Best Local Similarity 52.6%; Pred. No. 1.1e+02;

Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

17 KPIDNTLYPIADDENTLES 35

666 KPIPNRAYVIXDDEVLEA 684

RESULT 19

outer layer protein VP3 - simian rotavirus SA11 (strain SA11-FEM)

C/Species: simian rotavirus SA11

C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004

C/Accession: B31159

R/Nishikawa, K.; Taniguchi, K.; Torres, A.; Hoshino, Y.; Green, K.; Kapikian, A.Z.; Chan

C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C/Accession: B31159

C/Species: simian rotavirus SA11

J. Virol. 62, 4022-4026, 1988

A/Title: Comparative analysis of the VP3 gene of divergent strains of the rotaviruses si

A/Reference number: A94694; MUID:89012172; PMID:2845121

A/Accession: B31159

A/Molecule type: genomic RNA

A/Residues: 1-776 <NIS>

A/Cross-references: UNIPROT:P17463

C/Genetics:

A/Map position: segment 4

C/Superfamily: rotavirus outer layer protein VP3

C/Keywords: glycoprotein; hemagglutinin; outer capsid protein

P/248-776/Product: outer layer protein VP3 #status predicted <VP3>

P/32,56,97,132,151,198,456,507,602/Binding site: carbohydrate (Asn) (covalent) #status p

Query Match 26.1%; Score 49; DB 1; Length 776;

Best Local Similarity 52.6%; Pred. No. 1.1e+02;

Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

17 KPIDNTLYPIADDENTLES 35

666 KPIPNRAYVIXDDEVLEA 684

RESULT 20

hypothetical outer capsid protein - simian rotavirus SA11

C/Species: simian rotavirus SA11

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C/Accession: S24410

R/Mattion, N.M.; Bates, M.K.

Arch. Virol. 120, 109-113, 1991

A/Title: Sequence of a rotavirus gene 4 associated with unique biologic properties.

A/Reference number: S24410; MUID:92028406; PMID:1656916

A/Accession: S24410

A/Status: preliminary

A/Molecule type: genomic RNA

A/Residues: 1-776 <MAT>

A/Cross-references: UNIPROT:Q68802; UNIPROT:Q71293; EMBL:X57319

C/Superfamily: rotavirus outer layer protein VP3

Query Match 26.1%; Score 49; DB 2; Length 776;

Best Local Similarity 52.6%; Pred. No. 1.1e+02;

Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

17 KPIDNTLYPIADDENTLES 35

666 KPIPNRAYVIXDDEVLEA 684

RESULT 21

hypothetical protein SPAC22F3.1ac - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe

C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C/Accession: T38055; T38177; S62429

R/Liye, G.; Churcher, C.M.; Barrett, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, February 1995

A/Reference number: Z21765

A/Accession: T38055

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-26 <LY1>

A/Cross-references: UNIPROT:009779; EMBL:669219; PIDN:CAA93223.1; GSPDB:GN00066; SPDB:SP

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-26 <LY2>

A/Cross-references: EMBL:Z54285; NID:91008429; PIDN:CAA91079.2; GSPDB:GN00066; SPDB:SPAC

C/Genetics:

A/Map position: segment 4

C/Superfamily: rotavirus outer layer protein VP3

C/Keywords: glycoprotein; hemagglutinin; outer capsid protein

P/248-776/Product: outer layer protein VP3 #status predicted <VP3>

P/32,56,97,132,151,198,456,507,602/Binding site: carbohydrate (Asn) (covalent) #status p

Query Match 26.1%; Score 49; DB 2; Length 776;

Best Local Similarity 52.6%; Pred. No. 1.1e+02;

Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

17 KPIDNTLYPIADDENTLES 35

666 KPIPNRAYVIXDDEVLEA 684

RESULT 12
AE2254
hypothetical protein alx388 [imported] - Nostoc sp. (strain PCC 7120)
C/Species: Nostoc sp. PCC 7120
A/Notes: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AE2254
R/Kanehisa, T.; Nakamura, Y.; Mol, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriuchika, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Ref. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena*
A/Reference number: AB1807, MIMD:21595285, PMID:11759840
A/Accession: AE2254
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-908 <KUR>
A/Cross-references: UNIPROT:Q8Y6Z, GB:BA000019, PIDN:BAF5287.1, PID:G17132721, GSPDB:C
A/Experimental source: strain PCC 7120
C/Genetics:
A/Genetic: alx388

Query Match 26.6%; Score 50; DB 2; Length 908;
Best Local Similarity 72.7%; Pred. No. 92;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 19 IDNTLYFIAD 29
:|||||:
Db 795 VDNLYEVAND 805

RESULT 13
T16604
hypothetical protein K10B2.5 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T16604
R/Miller, N.
Submitted to the EMBL Data Library, June 1995
A/Description: The sequence of C. elegans cosmid K10B2.
A/Reference number: 218545
A/Accession: T16604
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-11009 <MIL>
A/Cross-references: UNIPROT:Q09994; EMBL:U28730; NID:G860694; PID:G860699; PIDN:AAA68262
A/Experimental source: strain Bristol N2
C/Genetics:
A/Genetic: CDSF:K10B2.5
A/Introns: 29/3; 126/1; 175/2; 226/2; 266/1; 328/2; 389/2; 527/3; 732/1; 790/3; 982/2

Query Match 26.3%; Score 49.5; DB 2; Length 1009;
Best Local Similarity 37.5%; Pred. No. 1.2e+02;
Matches 12; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

QY 3 AEPVNDNCINFAVKFIDNTLYFIADDENL 34
:|||||:
Db 109 SEPMQDNKEVVTTFIDSM---IDHBEYE 137

RESULT 14
E97088
beta-xyloridase, family 43 glycosyl hydrolase CAC1529 [imported] - *Clostridium acetobutylicum*
C/Species: *Clostridium acetobutylicum*
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: E97088
R/Nolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.U.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*
A/Reference number: A96900, MIMD:21359325, PMID:21359325
A/Accession: E97088

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-327 <KUR>
A/Cross-references: UNIPROT:Q971W1; GB:AE001437; PIDN:AAK79496.1; PID:G15024478; GSPDB:C
A/Experimental source: *Clostridium acetobutylicum* ATCC824
C/Genetics:
A/Genetic: CAC1529
C/Superfamily: Streptomyces chartreusis alpha-L-arabinofuranosidase II

Query Match 26.1%; Score 49; DB 2; Length 327;
Best Local Similarity 32.6%; Pred. No. 43;
Matches 15; Conservative 6; Mismatches 13; Indels 12; Gaps 2;

QY 3 AEPV-----DNCINFAVKFIDNT--LYFIADDENL 36
:|||||:
Db 53 AEPVDVWRHRESGEMNLTPAPRHHTNGAWTYIFAPADKNIED 98

RESULT 15
A82890
hypothetical protein UH451 [imported] - *Ureaplasma urealyticum*
C/Species: *Ureaplasma urealyticum*
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C/Accession: A82890
R/Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, B.Y.; Cassell, G.H.
Submitted to Genbank, February 2000
A/Description: The complete sequence of *Ureaplasma urealyticum*. Alternate views of a min
A/Reference number: A82870
A/Accession: A82890
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-338 <GLA>
A/Cross-references: GB:AE002141; GB:AF222894; NID:G6899434; PIDN:AAF30863.1; GSPDB:GN001
A/Experimental source: serovar 3; biovar 1
C/Genetics:
A/Genetic: UH451
A/Genetic code: GGC3

Query Match 26.1%; Score 49; DB 2; Length 338;
Best Local Similarity 32.4%; Pred. No. 44;
Matches 11; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 3 AEPVNDNCINFAVKFIDNTLYFIADDENL 36
:|||||:
Db 225 AQLVDECLAPQSSVFNNEXFIEBYHIOPD 258

RESULT 16
H96911
uroporphyrinogen III synthase [imported] - *Clostridium acetobutylicum*
C/Species: *Clostridium acetobutylicum*
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: H96911
R/Nolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.U.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*
A/Reference number: A96900, MIMD:21359325, PMID:21359325
A/Accession: H96911
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-490 <KUR>
A/Cross-references: UNIPROT:Q97WU3; GB:AE001437; PIDN:AAK78083.1; PID:G15022922; GSPDB:G
A/Experimental source: *Clostridium acetobutylicum* ATCC824
C/Genetics:
A/Genetic: CAC0098
C/Superfamily: bifunctional uroporphyrin-III C-methyltransferase/uroporphyrinogen-III sy

Query Match 26.1%; Score 49; DB 2; Length 490;
Best Local Similarity 45.8%; Pred. No. 66;
Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 3 AEPVNDNCINFAVKFIDNTLYFI 26

Db 800 EKIDLRCSYSLINIKIHIHYKXMDLFTYTRDDENISS 840

RESULT 3

hypothetical protein F31A3.5 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: 129700

R/Murray, J., Le, T.T.

A/Description: The sequence of *C. elegans* cosmid F31A3.

A/Reference number: 22067

A/Accession: 129700

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-780 <MOR>

A/Cross-references: UNIPROT:P09057, EMBL:U58742, PDB:1AAB36859.1, GSPDB:GNO0028, CESP:F3

A/Experimental source: strain Bristol N2; clone F31A3

C/Genetics:

A/Map position: X

A/Initiators: 48/2; 137/2; 188/3; 261/3; 312/2; 370/3; 452/2; 486/3; 593/1; 615/2; 705/3

C/Superfamily: *Caenorhabditis elegans* hypothetical protein F31A3.5

Query Match 29.3%; Score 56; DB 2; Length 780;

Best Local Similarity 40.0%; Pred. No. 12;

Matches 12; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Db 49 PVEDNCINFMKFIIDNTLYFIADDENL 34

5 PVEDNCINFMKFIIDNTLYFIADDENL 34

49 PVEDNCINFMKFIIDNTLYFIADDENL 34

5 PVEDNCINFMKFIIDNTLYFIADDENL 34

49 PVEDNCINFMKFIIDNTLYFIADDENL 34

5 PVEDNCINFMKFIIDNTLYFIADDENL 34

49 PVEDNCINFMKFIIDNTLYFIADDENL 34

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5 PVEDNCINFMKFIIDNTLYFIADDENL 34

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49 PVEDNCINFMKFIIDNTLYFIADDENL 34

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49 PVEDNCINFMKFIIDNTLYFIADDENL 34

5 PVEDNCINFMKFIIDNTLYFIADDENL 34

49 PVEDNCINFMKFIIDNTLYFIADDENL 34

5 PVEDNCINFMKFIIDNTLYFIADDENL 34

49 PVEDNCINFMKFIIDNTLYFIADDENL 34

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2005, 12:16:10 / Search time 38 Seconds
(without alignments)
91.153 Million cell updates/sec

Title: US-09-711-896a-1

Perfect score: 188
Sequence: 1 MAEPVEDNCINFAVAKRFIDNTLYPIAEDDNLSD 36

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: EIR_79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110	58.5	192	2	S60226
2	62.5	33.2	1398	2	H71606
3	56	29.8	780	2	T29700
4	55	29.3	275	2	G89961
5	55	29.3	687	2	S53485
6	53	28.2	365	2	B81307
7	52.5	27.9	212	2	G97866
8	52	27.7	736	2	T00023
9	51	27.1	647	2	T28214
10	50	26.6	302	2	T38789
11	50	26.6	536	2	A56590
12	50	26.6	908	2	AE2254
13	49.5	26.3	1009	2	T16604
14	49	26.1	327	2	E97088
15	49	26.1	338	2	A82890
16	49	26.1	490	2	H56911
17	49	26.1	747	1	VPXR43
18	49	26.1	776	1	VPXR43
19	49	26.1	776	1	VPXR43
20	49	26.1	776	1	VPXR43
21	49	26.1	1628	2	T38055
22	48.5	25.8	285	2	T09308
23	48.5	25.8	299	2	JC4374
24	48.5	25.8	384	2	F81354
25	48.5	25.8	464	1	MZVZG1
26	48.5	25.8	1218	2	S71376
27	48.5	25.8	3712	2	S18253
28	48	25.5	209	2	H90128
29	48	25.5	480	2	T34102

30	47.5	25.3	284	2	A83688	hypothetical prote
31	47.5	25.3	367	2	T19337	hypothetical prote
32	47.5	25.3	482	2	B31795	collagen alpha 1(X
33	47.5	25.3	532	2	T02539	hypothetical prote
34	47.5	25.3	673	2	T15551	hypothetical prote
35	47.5	25.3	888	2	S28791	collagen alpha 1(X
36	47.5	25.3	1435	2	S54637	DNA polymerase III
37	47.5	25.3	1435	2	C90596	hypothetical prote
38	47.5	25.3	1806	1	CGHUIE	collagen alpha 1(X
39	47.5	25.0	250	2	S69031	hypothetical prote
40	47	25.0	316	2	S75062	transcription regu
41	47	25.0	357	2	T38405	hypothetical prote
42	47	25.0	443	1	AJCLQA	glutamate-ammonia
43	47	25.0	468	2	B72351	clostridial-relate
44	47	25.0	502	2	T29729	hypothetical prote
45	47	25.0	571	2	S68356	pept protein - Sta

ALIGNMENTS

RESULT 1
S60226
CYTOKINE IGIF - mouse
C/Species: Mus musculus (house mouse)
C/Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C/Accession: S60226
R/Okamura, H., Teuscher, H., Komatsu, T., Yutsudo, M., Hakura, A., Tanimoto, T., Torigoe, Nature 378, 88-91, 1995
A/Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A/Reference number: S60226; MUID:96061009; PMID:7477296
A/Accession: S60226
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-192 <OK>
A/Cross-references: UNIPROT:P70380; EMBL:D49949; NID:G1064822; PIDD:BA08705.1; PID:G106
C/Superfamily: Mus musculus cytokine IGIF

Query Match 58.5% Score 110; DB 2; Length 192;
Best Local Similarity 66.7%; Pred. No. 9.1e-08;
Matches 20; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 EDNCINFAVAKRFIDNTLYPIAEDDNLSD 36
DB 6 EDSCNFKEMFIDNTLYPIEENGDLSD 35

RESULT 2

H71606
Hypothetical protein PFB0755w - malaria parasite (Plasmodium falciparum)
C/Species: Plasmodium falciparum
C/Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
R/Gardner, M.J., Tetteh, H., Carucci, D.J., Cummings, L.M., Aravind, L., Koonin, E.V., Petteh, M., Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O., Smith, H.O. Science 282, 1126-1132, 1998
A/Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A/Reference number: A71600; MUID:99021743; PMID:9804551
A/Accession: H71606
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-1398 <GAR>
A/Cross-references: UNIPROT:O96244; GB:AE001416; GB:AE001362; NID:G3845268; PIDD:AACT194
A/Experimental source: clone 3D7
A/Genes: PFB0755w

Query Match 33.2% Score 62.5; DB 2; Length 1398;
Best Local Similarity 31.7%; Pred. No. 2.7;
Matches 13; Conservative 8; Mismatches 11; Indels 9; Gaps 1;

QY 4 EPVEDNCINFAVAKRFIDNTLYPIAEDDNLSD 35

FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-896-501A-2

Query Match 100.0%; Score 188; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MAAPEVDNCINFAMKFIIDNTLYFIADDDNLESD 36
DB 1 MAAPEVDNCINFAMKFIIDNTLYFIADDDNLESD 36

RESULT 5

US-08-832-180-9
Sequence 9, Application US/08832180
Patent No. 6214584

GENERAL INFORMATION:

APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUDO
APPLICANT: USHIO, Shimpel
APPLICANT: TORIGOE, Kakui
APPLICANT: TANIMOTO, Tadao
APPLICANT: OKAMURA, Haruki
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,180
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,191
FILING DATE:

APPLICATION NUMBER: JP 304,203/94
FILING DATE: No. 6214584ember 15, 1994
APPLICATION NUMBER: 10048102
FILING DATE: September 18, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: USHIO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-832-180-9

Query Match 100.0%; Score 188; DB 3; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MAAPEVDNCINFAMKFIIDNTLYFIADDDNLESD 36
DB 1 MAAPEVDNCINFAMKFIIDNTLYFIADDDNLESD 36

RESULT 6

US-10-105-080-4
Sequence 4, Application US/10105080
Patent No. 6800479

GENERAL INFORMATION:

APPLICANT: SAMYANG GENEX CORPORATION
APPLICANT: RECOMBINANT ADENOVIRUSES EXPRESSING INTERLEUKIN-18 PROTEIN AND
TITLE OF INVENTION: GENE THERAPY USING THEM
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/105,080
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: KR 10-2001-78296
PRIOR FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4
LENGTH: 193
TYPE: PRT
ORGANISM: Human interleukin-18 precursor mutant
US-10-105-080-4

Query Match 100.0%; Score 188; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MAAPEVDNCINFAMKFIIDNTLYFIADDDNLESD 36
DB 1 MAAPEVDNCINFAMKFIIDNTLYFIADDDNLESD 36

RESULT 7

US-09-949-016-6095
Sequence 6095, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6095
LENGTH: 193

TYPE: PRT
ORGANISM: Human
US-09-949-016-6095

Query Match 100.0%; Score 188; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEPVEDNCINFVAMKFIIDNTLYFIAEDDENLESD 36
DB 1 MAEPVEDNCINFVAMKFIIDNTLYFIAEDDENLESD 36

RESULT 8

US-09-597-576-2
Sequence 2, Application US/09597576
Patent No. 6432678
GENERAL INFORMATION:
APPLICANT: Alexander Taylor
APPLICANT: Han Trinh
TITLE OF INVENTION: MACACA CYNOMOLGUS IL18
FILE REFERENCE: GP-70629
CURRENT APPLICATION NUMBER: US/09/597,576
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 60/140,140
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 193
TYPE: PRT
ORGANISM: MACACA CYNOMOLGUS
US-09-597-576-2

Query Match
Best Local Similarity 95.2%; Score 179; DB 4; Length 193;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEPVEDNCINFVAMKFIIDNTLYFIAEDDENLESD 36
DB 1 MAEPVEDNCINFVAMKFIIDNTLYFIAEDDENLESD 36

RESULT 9

US-09-917-265A-2
Sequence 2, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Borroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 133
TYPE: PRT
ORGANISM: Felis catus
FEATURE:
NAME/KEY: misc.feature
LOCATION: (119)..(119)
OTHER INFORMATION: The 'Xaa' at location 119 stands for Lys, or Asn.
US-09-917-265A-2

Query Match
Best Local Similarity 74.2%; Score 139.5; DB 4; Length 133;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MAEPVEDNCINFVAMKFIIDNTLYFIAEDDENLESD 36
DB 1 MTAIPVDD-CINPVGKFIIDNTLYFVADSDENLESD 35

RESULT 10

US-09-917-265A-8
Sequence 8, Application US/09917265A
Patent No. 6818444
GENERAL INFORMATION:
APPLICANT: Wonderling, Ramani S.
APPLICANT: Borroughs, Karen L.
TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: IM-5
CURRENT APPLICATION NUMBER: US/09/917,265A
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 60/223,016
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 192
TYPE: PRT
ORGANISM: Felis catus
US-09-917-265A-8

Query Match
Best Local Similarity 74.2%; Score 139.5; DB 4; Length 192;
Matches 27; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MAEPVEDNCINFVAMKFIIDNTLYFIAEDDENLESD 36
DB 1 MTAIPVDD-CINPVGKFIIDNTLYFVADSDENLESD 35

RESULT 11

US-09-445-724B-2
Sequence 2, Application US/09445724B
Patent No. 6600020
GENERAL INFORMATION:
APPLICANT: OKANO, FUMIYOSHI
TITLE OF INVENTION: CANINE INTERLEUKIN 18, CANINE INTERLEUKIN 1 CONVERTING
TITLE OF INVENTION: ENZYME, DNA SEQUENCES ENCODING THESE, INTERLEUKIN 18
TITLE OF INVENTION: PRODUCTION METHOD AND CANINE IMMUNE DISEASE REMEDY
FILE REFERENCE: 2109-15
CURRENT APPLICATION NUMBER: US/09/445,724B
CURRENT FILING DATE: 1999-12-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 193
TYPE: PRT
ORGANISM: Caninus sp.
US-09-445-724B-2

Query Match
Best Local Similarity 70.2%; Score 132; DB 4; Length 193;
Matches 25; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAEPVEDNCINFVAMKFIIDNTLYFIAEDDENLESD 36
DB 1 MATNLIEDNCINLVKMKFVNNTLYFKASDGLSD 36

RESULT 12

US-09-445-724B-6
Sequence 6, Application US/09445724B
Patent No. 6600020
GENERAL INFORMATION:
APPLICANT: OKANO, FUMIYOSHI
TITLE OF INVENTION: CANINE INTERLEUKIN 18, CANINE INTERLEUKIN 1 CONVERTING
TITLE OF INVENTION: ENZYME, DNA SEQUENCES ENCODING THESE, INTERLEUKIN 18
TITLE OF INVENTION: PRODUCTION METHOD AND CANINE IMMUNE DISEASE REMEDY
FILE REFERENCE: 2109-15
CURRENT APPLICATION NUMBER: US/09/445,724B
CURRENT FILING DATE: 1999-12-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1

TYPE: PRT

; SOFTWARE: PatentIn version 3.0


```

ADDRESSSES: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Avenue, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1888  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/089,397A  
FILING DATE: 07-JUL-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: ADLER, REID G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 29311-20003.03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 747 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-089-397A-16
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Query Match 26.1% Score 49 DB 3 Length 747;
Best Local Similarity 52.6%; Pred. No. 77;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 663 KFIPIRAIRVIKDDVEEA 681

OY 17 KEIDNTLYFIADDEENLES 35

RESULT 21
US-07-603-133B-17
Sequence 17, Application US/07603133B
Patent No. 5298244
GENERAL INFORMATION:
APPLICANT: Redmond, Mark J.
APPLICANT: Ijaz, Mohammed K.
APPLICANT: Parker, Michael D.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Robins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9313-0004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250

```

      TELEFAX: (415) 337-2951
      TELEX: 706141
      INFORMATION FOR SEQ ID NO: 17:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 776 amino acids
      TYPE: AMINO ACID
      STRANDEDNESS: unknown
      TOPOLOGY: unknown
      MOLECULE TYPE: protein
      US-07-603-1338-17

Query Match      25.1%; Score 49; DB 1; Length 776;
Beet Local Similarity 52.6%; Pred. No. 81;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy      17      KEIDNTLYFIIDDEENES 35
      |||      .|.|||.|||.
Db      666      KEIPNRAVYIKDDVELEA 684

```

RESULT 22
 US-07-603-133B-20
 Sequence 20 Application US/07603133B
 Patent No. 5298244
 GENERAL INFORMATION:
 APPLICANT: Redmond, Mark J.
 APPLICANT: Ijaz, Mohammed K.
 APPLICANT: Parker, Michael D.
 TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
 TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster
 STREET: 545 Middlefield Road, Suite 200
 CITY: Menlo Park
 STATE: CA
 COUNTRY: USA
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/603.133B
 FILING DATE: 19901025
 CLASSIFICATION: 42A
 ATTORNEY/AGENT INFORMATION:
 NAME: Robins, Roberta L.
 REGISTRATION NUMBER: 33,208
 REFERENCE/DOCKET NUMBER: 9313-0004.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 327-7250
 TELEFAX: (415) 327-2951
 TELEX: 7061141
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 776 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-603-133B-20
 Query Match 26.1%, Score 49, DB 1, Length 776;
 Best Local Similarity 52.6%, Pred. No. 81,
 Matches 10, Conservative 3, Mismatches 6, Indels 0, Gaps 0,
 17 KEIDENTIFYABDENIES 35
 ||| | :||| :
 666 KFLPNRAIVRIKDEVLVLA 684

RESULT 23

US-08-089-397A-15
 / Sequence 15, Application US/08089397A
 / Patent No. 6086880
 / GENERAL INFORMATION:
 / APPLICANT: SABAR, MARTA I. J.
 / APPLICANT: FRENCHICK, PATRICK J.
 / APPLICANT: POTTER, ANDREW A.
 / APPLICANT: IGAN, MOHAMMAD K.
 / APPLICANT: GILCHRIST, JAMES B.
 / APPLICANT: REDMOND, MARK J.
 / TITLE OF INVENTION: ROTAVIRUS VACCINES
 / NUMBER OF SEQUENCES: 24
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: MORRISON & FORSTER
 / STREET: 2000 Pennsylvania Avenue, NW
 / CITY: Washington
 / STATE: DC
 / COUNTRY: USA
 / ZIP: 20006-1888
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/089,397A
 / FILING DATE: 07-JUL-1993
 / CLASSIFICATION: 530
 / ATTORNEY/AGENT INFORMATION:
 / NAME: ADLER, REID G.
 / REGISTRATION NUMBER: 30,988
 / REFERENCE/DOCKET NUMBER: 29311-20003.03
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (202) 887-1500
 / TELEFAX: (202) 887-0763
 / INFORMATION FOR SEQ ID NO: 15:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 776 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: unknown
 / TOPOLOGY: unknown
 / MOLECULAR TYPE: protein
 / US-08-089-397A-15

Query Match 26.1%; Score 49; DB 3; Length 776;
 Best Local Similarity 52.6%; Pred. No. 81;
 Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 17 KPIDNTLYPIADNDENLES 35
 DB 666 KFIIPNAYVINDVLEA 684

RESULT 24
 US-07-991-867B-2
 / Sequence 2, Application US/07991867B
 / Patent No. 5476781
 / GENERAL INFORMATION:
 / APPLICANT: MOYER, Richard W.
 / APPLICANT: Hall, Richard L.
 / APPLICANT: Gruidl, Michael E.
 / TITLE OF INVENTION: No. 5476781e1 Entomopoxvirus Expression System
 / NUMBER OF SEQUENCES: 66
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: David R. Saliwanchik
 / STREET: 2421 N.W. 41st Street, Suite A-1
 / CITY: Gainesville
 / STATE: FL
 / COUNTRY: USA
 / ZIP: 32606
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: IBM PC compatible
 / SOFTWARE: Patentin Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/07/991,867B
 / FILING DATE: 19-FEB-1991
 / CLASSIFICATION: 530
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Saliwanchik, David R.
 / REGISTRATION NUMBER: 31,794
 / REFERENCE/DOCKET NUMBER: UP114.C3
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 904-375-8100
 / TELEFAX: 904-372-5800
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 464 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULAR TYPE: protein
 / US-07-991-867B-2

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/991,867B
 FILING DATE: 12-DEC-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO 92/14818
 FILING DATE: 12-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,685
 FILING DATE: 30-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/657,584
 FILING DATE: 19-FEB-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: UP114.C3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 464 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 US-07-991-867B-2

Query Match 25.8%; Score 48.5; DB 1; Length 464;
 Best Local Similarity 57.9%; Pred. No. 51;
 Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVAMKE---IDNTLYPI 26
 DB 20 INFMSMLPFPSKIDNNVYPI 38

RESULT 25
 US-08-107-755A-2
 / Sequence 2, Application US/08107755A
 / Patent No. 5721352
 / GENERAL INFORMATION:
 / APPLICANT: MOYER, Richard W.
 / APPLICANT: Hall, Richard L.
 / APPLICANT: Gruidl, Michael E.
 / TITLE OF INVENTION: No. 5721352e1 Entomopoxvirus Expression System
 / NUMBER OF SEQUENCES: 40
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: David R. Saliwanchik
 / STREET: 2421 N.W. 41st Street, Suite A-1
 / CITY: Gainesville
 / STATE: Florida
 / COUNTRY: U.S.A.
 / ZIP: 32606
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: IBM PC compatible
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/107,755A
 / FILING DATE: 19-AUG-1993
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/827,658
 / FILING DATE: 30-JAN-1992
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/657,584
 / FILING DATE: 19-FEB-1991
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UP114.C2
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-107-755A-2

Query Match 25.8%; Score 48.5; DB 1; Length 464;
Best Local Similarity 57.9%; Pred. No. 51;
Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVANKF---IDNTLYFI 26
20 INFMSMLFPSKIDNMYFI 38

Db

RESULT 26
US-08-544-332-2
Sequence 2, Application US/08544332
Patent No. 5935777
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H.
REGISTRATION/DOCKET NUMBER: 35,746
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-544-332-2

Query Match 25.8%; Score 48.5; DB 2; Length 464;
Best Local Similarity 57.9%; Pred. No. 51;
Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVANKF---IDNTLYFI 26
20 INFMSMLFPSKIDNMYFI 38

Db

RESULT 27
US-09-370-861A-2
Sequence 2, Application US/09370861A
Patent No. 6410221
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 6410221el Entomopoxvirus Expression System
FILE REFERENCE: UP114.C4.D1
CURRENT APPLICATION NUMBER: US/09/370,861A
CURRENT FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 07/991,867
PRIOR FILING DATE: 1992-12-07
PRIOR APPLICATION NUMBER: US 08/107,755
PRIOR FILING DATE: 1993-08-19
PRIOR APPLICATION NUMBER: WO 92/14818
PRIOR FILING DATE: 1992-02-12
PRIOR APPLICATION NUMBER: US 07/827,685
PRIOR FILING DATE: 1992-01-30
PRIOR APPLICATION NUMBER: US 07/657,584
PRIOR FILING DATE: 1991-02-19
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 464
TYPE: PRT
ORGANISM: Amasacta moorei entomopoxvirus
US-09-370-861A-2

Query Match 25.8%; Score 48.5; DB 4; Length 464;
Best Local Similarity 57.9%; Pred. No. 51;
Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 11 INFVANKF---IDNTLYFI 26
20 INFMSMLFPSKIDNMYFI 38

Db

RESULT 28
US-09-134-000C-6731
Sequence 6731, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 6731
LENGTH: 93
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-6731

Query Match 25.5%; Score 48; DB 4; Length 93;
 Best Local Similarity 42.3%; Pred. No. 8.8;
 Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAAREVEDNCFVAMKPFIDNTLYPI 26
 DB 16 MLSPDENILISFVGIVFIDNLYLLI 41

RESULT 29
 US-09-248-796A-20803
 Sequence 20803, Application US/09248796A
 Patent No. 6747137
 GENERAL INFORMATION:

APPLICANT: Keith Weinstein et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 FILE REFERENCE: 107196.132
 CURRENT APPLICATION NUMBER: US/09/248,796A
 CURRENT FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: US 60/096,409
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO 20803
 LENGTH: 520
 TYPE: PRT
 ORGANISM: Candida albicans
 US-09-248-796A-20803

Query Match 25.5%; Score 48; DB 4; Length 520;
 Best Local Similarity 47.1%; Pred. No. 70;
 Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 20 DNTLYFIADDELDLESD 36
 DB 44 DNVLTFIKENEGIIIDPD 60

RESULT 30
 US-09-113-750A-3
 Sequence 3, Application US/09113750A
 Patent No. 6294176
 GENERAL INFORMATION:

APPLICANT: David E. Junker and Mark D. Cochran
 TITLE OF INVENTION: Recombinant Raccoonpox virus
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: John P. White
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/113,750A
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 55744
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 262-0400
 TELEFAX: (212) 664-0525
 TELEX: 422523

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 688 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-09-113-750A-3

Query Match 25.5%; Score 48; DB 3; Length 688;
 Best Local Similarity 43.5%; Pred. No. 98;
 Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 7 EDNCINLVAMKPFIDNTLYPIAD 29
 DB 222 EQICINLVKYPIDNVINFIROD 244

RESULT 31
 US-09-328-352-5474
 Sequence 5474, Application US/09328352
 Patent No. 6562958
 GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 FILE REFERENCE: GTC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO 5474
 LENGTH: 1039
 TYPE: PRT
 ORGANISM: Acinetobacter baumannii
 US-09-328-352-5474

Query Match 25.3%; Score 47.5; DB 4; Length 1039;
 Best Local Similarity 25.6%; Pred. No. 1.9e+02;
 Matches 11; Conservative 9; Mismatches 10; Indels 13; Gaps 1;

QY 5 PVENCINLVAMKPFIDNT-----LYFIADDELDLE 34
 DB 568 PKEDGILSVQIKVDASPIQSOKIGQVQYFLTGDKVD 610

RESULT 32
 US-09-919-497-56
 Sequence 56, Application US/09919497
 Patent No. 6773883
 GENERAL INFORMATION:

APPLICANT: Multer, George L.
 TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
 FILE REFERENCE: B0801/7225
 CURRENT APPLICATION NUMBER: US/09/919,497
 CURRENT FILING DATE: 2001-07-31
 PRIOR APPLICATION NUMBER: US 60/221,735
 PRIOR FILING DATE: 2000-07-31
 NUMBER OF SEQ ID NOS: 100
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 56
 LENGTH: 1806
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURES:
 NAME/KEY: UNSURE
 LOCATION: (758)..(758)
 OTHER INFORMATION: Xaa = any amino acid
 NAME/KEY: UNSURE
 LOCATION: (809)..(809)
 OTHER INFORMATION: Xaa = any amino acid
 US-09-919-497-56

Query Match 25.3%; Score 47.5; DB 4; Length 1806;
Best Local Similarity 23.3%; Pred. No. 3.8e+02;
Matches 11; Conservative 4; Mismatches 13; Indels 29; Gaps 1;

QY 6 VEDNCINFVAMKFTI-----DNTYFIAEDDENTESD 36
DB 1686 VEGSINMVMQMTFLKLTASARQNTYHCHQSAAMYDVSSGYKALRFLGSDNBEHNSYD 1745

RESULT 33
US-09-212-247C-4
Sequence 4, Application US/09212247C
Patent No. 6391603

GENERAL INFORMATION:

APPLICANT: POMEYUS, Markus, SUELBURGER, Harald, JOEFFKEN, Hans
Wolfgang; DOVAL, Jose Luis Revuelta; JIMENEZ, Alberto;
and GARCIA, Maria Angeles Santos
TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Goseypil
and the use thereof in microbial riboflavin
synthesis

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kell & Weinkauff

STREET: 1101 Connecticut Avenue

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage

COMPUTER: IBM AT-compatible, Pentium processor

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect version 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/212,247C

FILING DATE: 16-Dec-1998

CLASSIFICATION: <Unknown>

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 475 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-212-247C-4

Query Match 25.0%; Score 47; DB 3; Length 475;
Best Local Similarity 43.5%; Pred. No. 89;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 AAEVEDNCINFVAMKFTIDNTLY 24
DB 77 AASVALDSLINFAYKVFNNERY 99

RESULT 34
US-09-746-359A-39

Sequence 39, Application US/09746359A

Patent No. 6610286

GENERAL INFORMATION:

APPLICANT: Thompson, Penny

APPLICANT: Foster, Donald C.

APPLICANT: Xu, Wenfeng

APPLICANT: Madden, Karen L.

APPLICANT: Kelly, James D.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Blumberg, Hal

APPLICANT: Eagan, Maribeth A.

APPLICANT: Jaepers, Stephen R.

APPLICANT: Chandrasekhar, Yasmin A.

APPLICANT: No. 6610286ak, Julia E.

TITLE OF INVENTION: Method for Treating Inflammation

FILE REFERENCE: 99-108

CURRENT APPLICATION NUMBER: US/09/746,359A

CURRENT FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: 60/171,969

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/213,341

PRIOR FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 39

LENGTH: 514

TYPE: PRT

ORGANISM: Mus musculus

US-09-746-359A-39

Query Match 25.0%; Score 47; DB 4; Length 514;
Best Local Similarity 36.7%; Pred. No. 98;
Matches 11; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 4 EPEVEDNCINFVAMKFTIDNTLYFAEDDENTL 33
DB 273 EPEETITLNFITFSMLDTR--ISPKDML 300

RESULT 35
US-09-746-359A-37

Sequence 37, Application US/09746359A

Patent No. 6610286

GENERAL INFORMATION:

APPLICANT: Thompson, Penny

APPLICANT: Foster, Donald C.

APPLICANT: Xu, Wenfeng

APPLICANT: Madden, Karen L.

APPLICANT: Kelly, James D.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Blumberg, Hal

APPLICANT: Eagan, Maribeth A.

APPLICANT: Jaepers, Stephen R.

APPLICANT: Chandrasekhar, Yasmin A.

APPLICANT: No. 6610286ak, Julia E.

TITLE OF INVENTION: Method for Treating Inflammation

FILE REFERENCE: 99-108

CURRENT APPLICATION NUMBER: US/09/746,359A

CURRENT FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: 60/171,969

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/213,341

PRIOR FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 37

LENGTH: 546

TYPE: PRT

ORGANISM: Mus musculus

US-09-746-359A-37

Query Match 25.0%; Score 47; DB 4; Length 546;
Best Local Similarity 36.7%; Pred. No. 1.1e+02;
Matches 11; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 4 EPEVEDNCINFVAMKFTIDNTLYFAEDDENTL 33
DB 305 EPEETITLNFITFSMLDTR--ISPKDML 332

RESULT 36
US-08-895-522-4

Sequence 4, Application US/08895522

Patent No. 5858719

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Shah, Purvi

APPLICANT: Corley, Neil C.

TITLE OF INVENTION: HUMAN ATP-BINDING CASSETTE
TITLE OF INVENTION: TRANSPORT PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSES: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,522
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0336 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 575393
US-08-895-522-4

Query Match 25.0%; Score 47; DB 2; Length 694;
Best Local Similarity 43.5%; Pred. No. 1.4e+02;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

RESULT 37
US-09-195-391-4
Sequence 4, Application US/09195391
Patent No. 6080842
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN ATP-BINDING CASSETTE
TITLE OF INVENTION: TRANSPORT PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSES: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,391
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/895,522
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0336 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 575393
US-09-195-391-4

Query Match 25.0%; Score 47; DB 3; Length 694;
Best Local Similarity 43.5%; Pred. No. 1.4e+02;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

RESULT 38
US-07-603-133B-15
Sequence 15, Application US/07603133B
Patent No. 5298244
GENERAL INFORMATION:
APPLICANT: Redmond, Mark J.
APPLICANT: Ijaz, Mohamed K.
APPLICANT: Parker, Michael D.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSES: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Robins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9313-0004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
TELEFAX: (415) 327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 775 amino acids

TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-603-133B-15

Query Match 25.0%; Score 47; DB 1; Length 775;
Best Local Similarity 45.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 17 KFIIDNTLYFIADDDNLESD 36
||| : : : : :
Db 665 KFIPIKRAYRVLKDDVEVMEAD 684

RESULT 39
US-07-603-133B-16
Sequence 16, Application US/07603133B
Patent No. 5298244
GENERAL INFORMATION:

APPLICANT: Redmond, Mark J.
APPLICANT: Ijaz, Mohammed K.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:

NAME: Robins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9313-0004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
TELEFAX: (415) 327-2951
TELEX: 706141

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 775 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-603-133B-16

Query Match 25.0%; Score 47; DB 1; Length 775;
Best Local Similarity 45.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 17 KFIIDNTLYFIADDDNLESD 36
||| : : : : :
Db 665 KFIPIKRAYRVLKDDVEVMEAD 684

RESULT 40
US-09-538-092-323
Sequence 323, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:

APPLICANT: Glot, Lotc
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurataseqFormatter Version 0.9
SEQ ID NO 323
LENGTH: 818
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)..(0)
OTHER INFORMATION: Polypeptide Accession Number YGI229C
US-09-538-092-323

Query Match 24.7%; Score 46.5; DB 4; Length 818;
Best Local Similarity 25.5%; Pred. No. 2e+02;
Matches 13; Conservative 8; Mismatches 15; Indels 15; Gaps 2;

QY 1 MAAPVEDNDCIN-----FVAMKFIIDNTLYFIAB-DDENLESD 36
||| : : : : :
Db 498 ITSNTLDEKCNNDNSNDNOKKQKIKKGFHNEIYSTFDSDDNIDDD 548

Search completed: May 13, 2005, 12:26:43
Job time : 43 secs